

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 6, 2003, 02:31:15 / Search time 142 Seconds
(without alignments)
2475.011 Million cell updates/sec

Title: US-08-908-453-1

Perfect score: 6046

Sequence: 1 MHVNIHPOLQTMVEQWQMR.....AFNGSWSTKTNWLFHAVRHY 1146

Scoring table:

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Ygapop 10.0	Ygapext 0.5
Fgapop 6.0	Fgapext 7.0
Delop 6.0	Delext 7.0

Searched: 441362 segs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:*

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- 2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PTCUS.COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	6046	100.0	3504	4	US-08-857-076-47 Sequence 47, Appl
2	1089	18.0	3207	1	US-08-162-081B-35 Sequence 35, Appl
3	1089	18.0	3207	2	US-08-780-872-35 Sequence 35, Appl
4	1089	18.0	3207	4	US-08-085-957-35 Sequence 35, Appl
5	1082	17.9	3240	1	US-08-162-081B-34 Sequence 34, Appl
6	1082	17.9	3240	4	US-08-780-872-34 Sequence 34, Appl
7	1082	17.9	3240	4	US-08-085-957-34 Sequence 34, Appl
8	1079	17.8	3412	1	US-08-162-081B-32 Sequence 32, Appl
9	1079	17.8	3412	2	US-08-780-872-32 Sequence 32, Appl
10	1079	17.8	3412	4	US-08-085-957-32 Sequence 32, Appl
11	1038	17.2	3808	2	US-08-916-917-3 Sequence 3, Appl
12	1038	17.2	3808	2	US-08-972-631-3 Sequence 3, Appl

13	1038	17.2	3808	2	US-08-972-629-3	Sequence 3, Appl
14	1038	17.2	3808	2	US-08-972-630-3	Sequence 3, Appl
15	1038	17.2	3808	2	US-08-672-211-3	Sequence 3, Appl
16	1038	17.2	3808	3	US-09-225-170-3	Sequence 3, Appl
17	1035	17.1	3213	3	US-09-392-350-1	Sequence 1, Appl
18	1033	17.1	5220	2	US-08-777-405A-1	Sequence 1, Appl
19	1033	17.1	5220	2	US-08-977-871A-1	Sequence 1, Appl
20	1033	17.1	5220	2	US-08-225-951-1	Sequence 1, Appl
21	1031	17.1	3868	3	US-09-357-070-1	Sequence 1, Appl
22	1015	16.8	5162	2	US-08-916-917-13	Sequence 13, Appl
23	1015	16.8	5162	3	US-09-225-170-13	Sequence 13, Appl
24	1002	16.6	4134	2	US-08-817-090B-1	Sequence 1, Appl
25	1002	16.6	4137	2	US-08-817-090B-3	Sequence 1, Appl
26	639	10.6	5285	2	US-08-609-049A-29	Sequence 29, Appl
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28	624	10.3	5061	4	US-09-355-160D-1	Sequence 1, Appl
29	622.5	10.3	6831	2	US-08-609-049A-27	Sequence 27, Appl
30	622.5	10.3	6831	4	US-09-170-996-27	Sequence 27, Appl
31	551.5	9.1	3252	4	US-09-118-442-1	Sequence 1, Appl
32	551.5	9.1	3252	4	US-09-677-064-1	Sequence 1, Appl
33	257.5	4.3	393	1	US-08-162-081B-40	Sequence 40, Appl
34	257.5	4.3	393	2	US-08-780-872-40	Sequence 40, Appl
35	257.5	4.3	393	4	US-09-085-957-40	Sequence 40, Appl
36	257.5	4.3	2451	2	US-08-820-170A-29	Sequence 29, Appl
37	257.5	4.3	2451	3	US-09-055-659-29	Sequence 29, Appl
38	257.5	4.3	2451	4	US-09-273-555-29	Sequence 29, Appl
39	257.5	4.3	2451	4	US-09-565-538-29	Sequence 29, Appl
40	257.5	4.3	2451	4	US-09-661-468-29	Sequence 29, Appl
41	257.5	4.3	2487	2	US-08-820-170A-32	Sequence 32, Appl
42	257.5	4.3	2487	3	US-09-055-659-32	Sequence 32, Appl
43	257.5	4.3	2487	4	US-09-273-555-32	Sequence 32, Appl
44	257.5	4.3	2487	4	US-09-565-538-32	Sequence 32, Appl
45	257.5	4.3	2487	4	US-09-661-468-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-08-857-076-47
Sequence 47, Application US/08857076C
Patent No. 6225120
GENERAL INFORMATION:
APPLICANT: Ruvkun, Gary
APPLICANT: Kimura, Koutarou
APPLICANT: Patterson, Garth
APPLICANT: Ogy, Scott
APPLICANT: Paradis, Suzanne
APPLICANT: Tissenbaum, Heidi
APPLICANT: Morris, Jason
APPLICANT: Kowek, Allison
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
FILE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
FILE REFERENCE: 00786/351001
CURRENT APPLICATION NUMBER: US/08/857.076C
CURRENT FILING DATE: 1997-05-15
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 47
TYPE: DNA
ORGANISM: Caenorhabditis elegans
US-08-857-076-47
Alignment Scores:
Pred. No.: 0
Score: 6046.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4
Length: 3504
Matches: 1146
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0
US-08-908-453-1 (1-1146) x US-08-857-076-47 (1-3504)

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 DB 64 ATGCATGTTAACTTTTACATCCACAACTGCGAAGCATGTCGAGCAGTGGCAATGCCA 123
 QY 21 GUAARGProSerLeuGlu1nThrGlu1nGly1nGlySerLeuLeuGlu1nGly 40
 DB 124 GAACGCCCATCGCTGGAGACCGGAAATGGCAAGATCGCTGCTCGAATAATGAAAGT 183
 QY 41 Val1a1aAsp11e1LeuH1eThMetCysProPheGlyGluVal11eSerVal1a1aPheProTrp 60
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 QY 61 PheLeu1a1aAsnVal1a1aArgThSerLeuGlu11eLeuSerAspPheLeuH1eGlnLeu 80
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 QY 81 PheGluLeu11e1a1aProMetLeuSerTrpGly1nThrTySerVal1a1aProGlnAspTyVal 100
 DB 304 TTCGATATTGCTCCGATGGAAGTGGGAAACATATTCGTAAGCCACAGGATTATGTG 363
 QY 101 PheArgGlnLeuAsnAsnPheGlyGlu11eGluVal11ePheAsnAspAspGlnProLeu 120
 DB 364 TTCAGACAGTTGAATTAATTCGCGCAATTTGAAGTTATTTAAACGACATCAACCCCTG 423
 QY 121 SerTyLeuGluLeuH1eGly1nThrPheProMetLeuPheLeuTyGlnProAspGly11e 140
 DB 424 TCGAATTTAGAGCTCCACGCGACCTTCCAAATGCTTTCTTCCACACCTGATGGAAATA 483
 QY 141 AsnArgAspTyLeuGluLeuMetSerAsp11eSerH1eCysLeuGly1nTySerLeuAspTy 160
 DB 484 AACAGGATTAAGAATTAATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGT 543
 QY 161 LeuGluGlnSerLeuAspGlu1nGluLeuArgGlnPheArg1a1aSerLeuTrp1a1aArgTrp 180
 DB 544 CTGGAGAGAGAGCTCATGATGAGAACTCCGTCATTTCTGCTTCTCGGGCTCTCTAGC 603
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 QY 201 GlnTyLeuCysVal1a1aGlyLeuSerCysProTyAspLeuGlu1nSerTyVal1a1aVal 220
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 QY 221 TySerLeuSerTyGlnMetPheTrpArgGly1nArgGly1nGly1nGly1nGly1nGly1n 240
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 QY 241 TySerMetLeu11eGln1nGluPheAsnProAsnGlu1nThrProTySerLeuLeuH1e 260
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 QY 321 ArgArgGlnSerLeuVal1a1aLeuTyAspTyCysArgProTySerProLeuTyGluProH1e 340
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 DB 1864 TCGATGTGAGAGATACATTCATAAAGCAGAGCTGATTTGCTCATTTGTGCTCCGAA 1923
 QY 621 Leu1a1aPheVal1a1aThrAspArgGluLeuPheSerGluLeuTyVal1a1aMetLeuGluTy 640
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Qy IleAspCysCysLeuAsnProTyrAlaValLeuProMetGlyGluMetIleGlyIleIle 900
Db 2704 ATTGATTCGTTGTAACCCGTAACGAGTCTTCCAAATGGGGAATATGATGATTTAT 2763
Qy GlnValValProAsnCysLeuThrIlePheGluIleGlnValGlyThrGlyPheMetAsn 920
Db 2764 GAAAGTGGCCATATTGTAACCAATATTCGAGATTCAAGTTGGAACAGGATTCATGAT 2823
Qy ThrAlaValArgSerIleAspProSerPheMetAsnIleTrpIleArgIleGlnCysGly 940
Db 2824 ACAGCATGTCGAGATGATGATCTTCTGTTAAGAAATGATGATTCGGAACAAATGCGCA 2883
Qy IleGluAspGluValLeuLeuSerIleValAspSerThrIleAsnProIleGluIleIle 960
Db 2884 ATTGAAGTGAAGAAAGAAAGAAAGCAAAAGACTTACGAAATATCCATCAAGAAAGAG 2943
Qy IleAspAsnThrGlnAlaMetIleValIleTyrPheGluSerValAspArgPheLeuTyrSer 980
Db 2944 ATTGATATATCTCAAGCATGAAAGAAATATTTTGAAGTGTGATCGATTCCTATCTCG 3003
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Db 3004 TGTGTGATATATCTCAAGTTCACGTAATGGAATGGAATCAAGATCGTCAAGTATAT 3063
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Db 3064 CTGATGCTCACTGAGATGAGAAATATGTCACATGATTTCTGTCACATTTTGGGACAC 3123
Qy GlnIleValIleGluGlyIleGlnIleArgAspArgIleProPheIleLeuThrGlnHisPhe 1040
Db 3124 GGAAGACCAAACTGGATCCAGACGAGATCTCAACCGTTTATCTTAACCAACCACTTT 3183
Qy MetThrValIleArgSerGlyValSerValAspGlyAsnSerHisGlnLeuGlnHisPhe 1060
Db 3184 ATGACAGTGAATTCATCGAGTAAATCTGTGATGAGAAATTCGCAAGACTCAAAAAATTC 3243
Qy LysThrLeuCysValGluAlaIleTyrGluValMetTrpAsnAspArgAspLeuPheValSer 1080
Db 3244 AAAAGCTTATGCTGGAAGCTTACGAGATGATGATGATTAATCGAATTTGTTCTTTCC 3303
Qy LeuPheThrLeuMetLeuGlyMetGluLeuProGluLeuSerThrIleValIleAspLeuAsp 1100
Db 3304 TTGTTTCACTTGATCTCGAATGAGATGAGTTCCTGAGCTGTCTGACGAAAGCGGATTTGAT 3363

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Qy 1121 AlaGlyIleTyrGluGlnAlaPheAsnGlySerTrpSerThrIleValAsnTrpLeuPhe 1140
Db 3424 GCTGGAATCTAGAAAGAACCTTCAATGATGATGATGATCTTACCAAAACGAAATTGCTTTC 3483
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Db 3484 CACGCACTCAAAACACTAC 3501

RESULT 2
US-08-162-081B-35
/ Sequence 35, Application US/08162081B
/ Patent No. 5624492
/ GENERAL INFORMATION:
/ APPLICANT: Hiles, Ian Donald, Fry, Michael John, Dhand, Ritu
/ APPLICANT: Balas, Waterfield, Michael Derek, Parker, Peter
/ APPLICANT: Joseph, Orsu, Masayuki, Panayotou, George, Volintia,
/ APPLICANT: Stefano, Gout, Ivan Tarasovitch
/ TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
/ NUMBER OF SEQUENCES: 50
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Felife & Lynch
/ STREET: 805 Third Avenue
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10022
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
/ COMPUTER: IBM PS/2
/ OPERATING SYSTEM: PC-DOS
/ SOFTWARE: WordPerfect
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08162, 081B
/ FILING DATE: February 7, 1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/GB93/00761
/ FILING DATE: 13 April 1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Pasqualini, Patricia A.
/ REGISTRATION NUMBER: 34,894
/ REFERENCE/DOCKET NUMBER: LUD 5256
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 688-9200
/ TELEFAX: (212) 838-3884
/ INFORMATION FOR SEQ ID NO: 35:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3207 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-162-081B-35

Alignment Scores:
Pred. No.: 1,01e-119 Length: 3207
Score: 1089.00 Matches: 311
Percent Similarity: 46.37% Conservative: 219
Best Local Similarity: 27.21% Mismatches: 431
Query Match: 18.01% Gaps: 182
DB: 1 Gaps: 39

US-08-908-453-1 (1-1146) x US-08-162-081B-35 (1-3207)
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Db CCTCTCCATCAACCTTCTCAAGATGATCTTCTTACATTTCTGTACGTGTACCCCAAGAA 228
QY 108 GlyIleIleGluValIlePheAsnAspArgGlnProLeuSerIleLeuLeuIleGly 127
Db GCAGAAAGGAGAAATTTTGTATGATAACAAGACGCTTGTGACCTTGGGCTTTTTCAA 288
QY 128 ThrPheProMetLeuPheLeuTyrGlnProAspGlyIleAsnArgAspIleGlyLeuMet 147
Db -----CCCTTTTAAAGTAATTTGAACCAAGTAGGCAACCCGTGAAGAAAGATCCCAT 342
QY 148 SerAspIleSerHisCysLeuGlyTyrSerIleAspIleLeuGlnLeuSerIleAspGlu 167
Db CAGAAATGTGTTTGTCTATCGCATGCAAGTGTGAATTCGATATGCTTAAAGATCCA 402
QY 168 GluLeuArgGlnPheArgIleSerLeuTyrPalaArgThrIleLeuSerCysLeuThrArg 187
Db GAAGTACAGAGACTTCCGAGAAATATTCATGTTGTAAAGACCTGTGATCTTACG 462
QY 188 GlyLeu-----GluGlyThrSerHisTyrPalaPheProGlnGluGlnTyrLeuCys 204
Db GATCTTAATTCACCTCATAGTAGAGCAATGTATGTTTATCTTCCAAAT-----GTAGAA 516
QY 205 ValGlyGluSerCysProIleAspLeuGluSerIleValIleAlaIleAlaIleLeuSerTyr 224
Db TCTTACCAAGAACTGCAAGACATATATATTAATTTGATTAAGGCAATA--ATA 573
QY 225 GlnMetPheTyr-----ArgIleAspArgIleAlaGluIle 235
Db GTGGGATTTGGGTATAGTTTCTCCAAATATGACAAACAGAAAGTATCTGTGAATAATC 633
QY 236 AsnGlyValCys-----GluIleMetMetIleGlnIleGluPheAsnProAsnGlu 253
Db AACCATGACTGTGTGCAGAACAGTAATTTGCTGAAGCAATCAGG-----AAAAA 684
QY 254 ThrProIleSerIleLeuHisThrPheLeuTyrGlnMetArgIleAspValTyrAsp 273
Db ACTCGAAGTATGTTGCTTATCATCT-----GAAACAATAAATCTGTGTTTAAAGA 735
QY 274 ThrAspAspProAlaAspGluGlyTyrPheLeuGlnLeuAlaGlyArgThrThrPheVal 293
Db TATCAGGGCAAG-----TATATTTTAAAGTGTGTGATGTGATGATGATCTTC 783
QY 294 ThrAsnProAspValIleLeuThrSerTyrAspGlyValArgSerGluLeuGluSerTyr 313
Db CTAGAA--AAATATCTCTGAGTCACTATTAAGTATTAAGAGCTGTATATGCTTGGG 840
QY 314 ArgCysProGlyPheValValArgArgGlnSerLeuValLeuAspTyrCysArgPro 333
Db AGGATGCCCAATTTGATGCTGATGCTGCTAA----- 870
QY 334 LysProLeuTyrGlnProHisTyrValArgAlaHisGluArgIleLeuAlaLeuAspVal 353
Db GAAGGCTCTATCT-----CACTGCCAATGAGACTGT 903
QY 354 LeuSerValSerIleAspSerThrProIleGlnSerIleAsnSerArgMetValMetThr 373
Db TTTACATG-----CCATCATATTTCCAGACGCACTCCACAGCTACGCA 948
QY 374 AspPheArgProThrAlaSerLeuLysGlnValSerLeuThrAspLeuAspAlaAsnLeu 393
Db TATATGAATGAGAAACATCTACAAA-----TCCCTTGGGTTTAAATATGATGCACTC 1002
QY 394 MetIleArg-----ProValAsnIleSerGlyPheAspPhePro 406
Db AGAATATAAATCTTTGTGCAACCTATGTGAATGTAATCTGAGACATGTAC----- 1056
QY 407 AlaAspValAspMetTyrValArgIleGluPheSerValTyrValGlyThrLeuThrLeu 426
Db -----AAGATTTATGTTTGAACA-----GGATCTACCATGTGAGAGAACCTCTTA 1101
QY 427 AlaSerIle--SerThrThrIleValAlaAsnAlaGlnPheAlaIleTyrAspIleLysGluMet 445

Db 1102 TGTGATATGTGAACACTCAAGACTACTCTTGTCCATCCACAGTGAAT--GAATCG 1158
QY 446 TyrThrPheAspLeuTyrMetIleAspMetProProSerAla-----ValLeuSerIle 463
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QY 464 ArgValLeuTyrGlyValValIleLeuLysSerGlnGluPheGluValGlyTyrValAsn 483
Db TGTCTGTAAAGCGCAAGAGGTGCTTAAGAGAACCTGTCCATTTGGCTGGAGAAAT 1278
QY 484 MetSerLeuThrAspTyrPalaAspGluLeuArgGlnGlyGlnPheLeuPheHisLeuTyr 503
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QY 504 AlaProGluProThrAlaAsnArgSerArgIleGlyIleAsnGlyAlaArgIleGlyThr 523
Db ---CCAGTACCTCATGACTAGAAAGATTTGCTGAACCTTATTTGGTGT--ACTGGATCA 1392
QY 524 Asn-----AlaAlaValThrIleGluIleSerSerTyrGlyValArgVal 538
Db AATCCAAATTAAGAAATCTCCATGTTTATAGATTTGAGTTTACTGTTCAGCAGTGTGTA 1452
QY 539 ArgMetProSerGlnGlyGlnTyrThrThrIleValIleAspSerThrTyrThrGlu 558
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QY 567 TyrGlu-----SerCysIleArgAspProGly 575
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QY 576 TyrIleLysLeuGlnMetLeuValIleLysGlnSerGlyIleValLeuGlnGluAsp 595
Db TCTGAA-----ATCAGTACGAA 1638
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QY 633 GluLeuTyrValMetLeuGlnLysTyrLysProProSerValAlaAlaAlaLeuThrLeu 652
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QY 653 LeuGlyLysArgCysThrAspArgValIleArgLysPheAlaValAlaGluLysLeuAsnGlu 672
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Qy 1124 TyrGluGluAlaPheAsnGlySerIlySerThrIlySerThrAsnIleuPheHisAlaVal 1143
 Db 3127 ATGATGATGACACACCATGATGCTGCGACACAAACAAATGATGATCTTCCACACAT 3186
 Qy 1144 LysHisIlyr 1146
 Db 3187 AAGCAGCAT 3195
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 RESULT 3
 US-08-780-872-35
 ; Sequence 35, Application US/08780872
 ; Patent No. 5846824
 ; GENERAL INFORMATION:
 ; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
 ; APPLICANT: Balai, Waterfield, Michael Derek; Parker, Peter
 ; APPLICANT: Joseph, Olan; Masayuki; Panayotou, George; Volinia,
 ; APPLICANT: Stefano; Gout, Ivan; Tarasovitch
 ; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
 ; TITLE OF INVENTION: THEIR PREPARATION AND USE
 ; NUMBER OF SEQUENCES: 50
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Felte & Lynch
 ; STREET: 805 Third Avenue
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10022
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: Wordperfect
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/780, 872
 ; FILING DATE: 09-JAN-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/162, 081
 ; FILING DATE: February 7, 1994
 ; APPLICATION NUMBER: PCT/GB93/00761
 ; FILING DATE: 13 April 1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Pasqualini, Patricia A.
 ; REGISTRATION NUMBER: 34,894
 ; REFERENCE/DOCKET NUMBER: LUD 5256
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 688-3884
 ; TELEFAX: (212) 838-3884
 ; INFORMATION FOR SEQ ID NO: 35:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3207 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-780-872-35
 Alignment Scores:
 Pred. No.: 1,01e-119 Length: 3207
 Score: 1089.00 Matches: 311
 Percent Similarity: 46.37% Conservative: 219
 Best Local Similarity: 27.21% Mismatches: 431
 Query Match: 18.01% Indels: 182
 Db: 2 Gaps: 39
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 Db 115 GAGGCTACGTTAATATACATTAAGCATTAAGCATTAATTTAA-----GAAGCAAGAAATATC 168
 Qy 90 GlyThrIlySerValIlyProGluIlyAsp-----TyrValPheArgGluIleuAsnAsnPhe 107

Db CCTCCATCAACTTCTTCAAGTGAATCTTCACTTTTGTGAAGTTACCCAGAA 228
 Qy 108 GYGLVLLLEGLVALLLEPHEASNPARGINPROLEUSERLYSEUGLULEUHSGLY 127
 Db 229 GCAGAAAGGGAAGAAATTTTGTATGMAACAGACGCTTGTGACCTTGCGCTTTTCA 288
 Qy 128 ThrPheProMetLeuPheLeuTyrgInPcoAsrgLlLaAsnAArgAspLysGluMet 147
 Db 289 -----CCCTTTTAAAGTAATGTAACAGTAGGACCGACCGMAAATAATCTCAAT 342
 Qy 148 SerAspIleSerHisCysLeuGlyTygSerLeuAspLysLeuGluGluSerLeuAspGlu 167
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 Qy 168 GluLeuArgGlnPheArgAlaSerLeuTrpAlaArgThrLysLeuThrArg 187
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 Qy 188 GlyLeu-----GluGlyThrSerHisTygAlaPheProGluGluGlnTygLeuGly 204
 Db 463 GATCTTAATTCACCTCATGTAGAGCAATGTAATGTTATCTCCAAAT-----GTAGA 516
 Qy 205 ValGlyGluSerCysProLysAspLeuGluSerLysValLysAlaAlaLysLeuSerTyg 224
 Db 517 TCTTCAACAGAACTGCCAAGCACATATATTAATTAATGATTAAGCGCAATAA---ATA 573
 Qy 225 GlnMetPheTrp-----ArgLysArgLysAlaGluLe 235
 Db 574 GGGGGATTTGGGTAATAGTTTCTCCAAATTAATGACAAACAGAGATATCTGTGAATAAC 633
 Qy 236 AsnGlyValLys-----GluLysMetLysLleGlnLleGluPheAsnProAsnGlu 253
 Db 634 AACCATGACTGTGTCCAGAACAGTAATTCCTGAAGCAATCAG-----AAAAA 684
 Qy 254 ThrProLysSerLeuLeuHisThrPheLeuTygGluMetArgLysLeuAspValTygAsp 273
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 Db 736 TATCAGGGCAG-----TATATTTTAAAGTGTGAGATGATGATCTTC 783
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 Qy 334 LysProLeuTyrgInProHisTygValArgAlaHisGluArgLysLeuAlaLeuAspVal 353
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 Qy 374 AspPheArgProThrAlaSerLeuLysGlnValSerLeuTrpAspLeuAspAlaLeuLeu 393
 Db 949 TATATGAATGAGAAACATCTACAAA-----TCCCTTTGGGTATTAATAGTGACATC 1002
 Qy 394 MetLleArg-----ProValAsnLleSerLysGluPheAspPhePro 406
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Qy 446 TyrThrPheAspLeuTyrgMetLysAspMetProProSerAla-----ValLeuSerLle 463
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 Db 1279 ATAACTTGTTGATTACACAGATPCTACTATCTGAAAAAAGGCTTTGAATCTTTGG 1338
 Qy 504 AlaProGluProThrAlaAsnArgSerArgLleGlyGluAsnGlyAlaArgLleGlyThr 523
 Db 1339 ---CCAGTACCTCATGACTAGAGATTTGCTGAACCTTATTTGGTT---ACTGATCA 1392
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 Db 1393 AATCAAAATTAAGAAACCTCCANTGTTAGATGTGAGTTGACTGCTGACGAGTGGTA 1452
 Qy 539 ArgMetProSerGlnGlyGlnTygThrTygLeuValLysHisArgSerThrTrpThrGlu 558
 Db 1453 AAGTTCCAGATATGTCA-----GTGATGAAGAGCAATGCCAATGTGCTGTA 1500
 Qy 559 Thr-----LeuAsnLleMetGlyAspAsp 566
 Db 1501 TCCCGTAGACGAGATTAGTTATTTCCATGACGAGCTGAGTAAAGCTAGCTAGAGAC 1560
 Qy 567 TyrgLys-----SerCysLleArgAspProGly 575
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 Db 1621 TCTGAA-----ATCATGACGAA 1638
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 Qy 693 GluProArgAlaGlnSerGluValGlyMetLeuLeuThrArgAlaLeuCysAspTyg 712
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RESULT 4
US-09-085-957-35
; Sequence 35, Application US/09085957
; Patent No. 6274327
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Balaj, Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph, Otsu, Masayuki; Panayotou, George; Volinia,
; APPLICANT: Stefano, Gout, Ivan Iaroslavitch
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/085,957
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/780,872
; FILING DATE: 09-JAN-1997
; APPLICATION NUMBER: 08/162,081
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: PCT/GB93/00761
; FILING DATE: 13 April 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: LUD 5256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 838-3884
; TELEFAX: (212) 838-9200
; INFORMATION FOR SEO ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3207 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-085-957-35

Alignment Scores:
Pred. No.: 1,01e-119 Length: 3207
Score: 1089.00 Matches: 311
Percent Similarity: 46.37% Conservative: 219
Best Local Similarity: 27.21% Mismatches: 431
Query Match: 18.01% Indels: 182
DB: 4 Gaps: 39

US-08-908-453-1 (1-1146) x US-09-085-957-35 (1-3207)
QY 70 GluIleIlySerAspPheIlyHisGlnIleuPheGlnIleuIleAlaPrometIlyTrp 89
DB 115 GAGGCTTACGTTAATTAACATTAAGCATGAACATTAATTA-----GAAACAAAGAAATAC 168
QY 90 GlyThrIlySerValIlyProGlnIAsp-----TyrValPheArgGlnIleuAsnAspPhe 107

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Db CCTCCATCACTTCTCAAGATGATGATCTTCTACATTTTGGTAAGTTACCAAGAA 228
Qy 169
Qy 108 GylgluilegluValillepheasnasparglnProleuserlysleugluLeuhsgly 127
Db 229 GCAGAAAGGAGAAATTTTGTGATGAAACAGACGCTTGTGACCTTGGCTTTTCA 288
Qy 128 ThrPheProMetLeuPheLeuTyrglnProasparglIleasnargaspargluLeuMet 147
Db 289 -----CCCTTTTAAAGTAATTTGAACAGAGGACCGTGAAGAAAGATCTCTCAAT 342
Qy 148 SeraspIleSerHisCysleuglyTyrglnSerLeuaspIysleugluLeuSerLeuaspIu 167
Db 343 CGAAGAAATGGTTTGTCTATCGGCATGCGAGTGTGATGATTCGATTTGTTAAAGTCCA 402
Qy 168 GluLeuArglnPheArgIleSerLeuTPrAlaArgThrIlyleuThrCysleuThrArg 187
Db 403 GAAGTACAGACTCTCGAAGAAATATTCGAATGTTTGAAGACCTGTGATCTTTAG 462
Qy 188 GlyLeu-----GluGlyThrSerHisTyrglnPheProgluLeuGluGlyLeuTyrgln 204
Db 463 GATCTTAATTCACCTCATGATGAGCAATGATGTTTCTTCCAAAT-----GTAGA 516
Qy 205 ValGlyGluSerCysProlysnaspIysleuSerIysValIysAlaIysleuSerTyrg 224
Db 517 TCTTACCGAAGCTGCCAAGACATATATTAATTTGGATTAAGCGCAATA---ATA 573
Qy 225 GluMetPheTrp-----ArgIysArgIysAlaGluIle 235
Db 574 GTGGTCATTTGGGTATATAGTTTCTCCAAATAATGACAAACAGAAATATCTCTGAAATC 633
Qy 236 AsnGlyValCys-----GluIysMetMetIysIleGlnIleGluPheasnProasparg 253
Db 634 AACCATGACTGTGTCCAGAACAGTAATTCCTGGAAGCATCAG-----AAAAA 684
Qy 254 ThrProlysnaspIysleuHisThrPheLeuTyrglnMetArgIysleuaspValTyrg 273
Db 685 ACTCGAAGATGATGCTATCATCT-----GAACAACTMAAACTGTGTGTTAGAA 735
Qy 274 ThrAspAspProAlaaspIuGlyTyrgPheLeuGlnLeuAlaGlyArgThrPheVal 293
Db 736 TATCAGGGCAG-----TATATTTTAAAGTGTGATGATGATGATCTTC 783
Qy 294 ThrAsnProaspValIysleuThrSerTyrgaspGlyValArgSerGluLeuSerTyrg 313
Db 784 CTRAGAA---AAATATCTCTGAGTCACTTAAGTATATTAAGAGCTGTATATGCTTGG 840
Qy 314 ArgCysProGlyPheValValArgArgInSerLeuValleuIysaspTyrgCysArgPro 333
Db 841 AGGATGCCCAATTTGATGCTGATGCTGCTAA----- 870
Qy 334 LysProLeuTyrgIuProHisTyrgValArgAlaHisGluArgIysleuAlaLeuAspVal 353
Db 871 GAAAGCCTCTATCT-----CAACTGCCCAATGAGACTGT 903
Qy 354 LeuSerValSerIleaspSerThrProlysnaspIysleuSerIysaspMetValMetThr 373
Db 904 TTTCACATG-----CATCATATTCAGAGCATCTCCACAGCTAGCCCA 948
Qy 374 AspPheArgProThrAlaSerIleuTyrglnValSerLeuTPraspIysleuAspAlaLeu 393
Db 949 TATATGAATGAGAAACATCTACAAA-----TCCCTTGGGTATTAATATGTCAGCTC 1002
Qy 394 MetIleArg-----ProValAsnIleSerGlyPheAspPhePro 406
Db 1003 AGAATAAATTTCTTGTGCACCTATGTGAATGTAATTAATTCAGACATTCAC----- 1056
Qy 407 AlaaspValaspMetTyrglnValArgIleGluPheSerValTyrgValGlyThrLeuThrLeu 426
Db 1057 -----AAGATTATATGTTGACAA-----GGATCTACCATGAGAGAACCTT 1101
Qy 427 AlaSerIys---SerThrIlysnaspIysAlaAsnAlaGlnPheAlaIysTPraspIysGluMet 445
Db 1102 TGTGATTAATGTGAACACTCAAAAGATACCTTGTCCAAATCCAGGTGAAT---GAATGG 1158

Qy 446 TyrThrPheaspLeuTyrgMetIysaspMetProProSerAla-----ValleuSerIle 463
Db 1159 CTGAATTACGATATATATATCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1218
Qy 464 ArgValleuTyrgIlysnaspIysleuSerGluGluPheGluValGlyTyrgValAsn 483
Db 1219 TGTTCGTAAAGCGCAAGAGGTCCTTAAGAGAACACTGTCCATCTGCGCTGGGAAT 1278
Qy 484 MetSerLeuThrAspTPraspIysleuArgIleGlnGlyGlnPheLeuPheHisleuThr 503
Db 1279 ATAACTGTTTGTGATACAGATACCTGATATCTGCAAAAATGGCTTTGAATCTTTGG 1338
Qy 504 AlaProgluProThrAlaAsnArgSerArgIleGlyGluAsnGlyAlaArgIleGlyThr 523
Db 1339 ---CCAGTACCTCATGACTGAGACTGAAAGATTTGCTGAACCTTATGGTGT---ACTGGATCA 1392
Qy 524 Asn-----AlaAlaValThrIleGluIleSerSerTyrgIlyArgVal 538
Db 1393 AATCAAAATTAAGAAACCTCATGTTTATAGTTGAGTTGACTGGTTGACAGCATGTGGTA 1452
Qy 539 ArgMetProSerGlnGlyGlnTyrgThrTyrgLeuValIysHisArgSerThrTPraspIu 558
Db 1453 AAGTTTCCAGATATGTC-----GTGATGAAGAGCAAGCCAAATTTGCTGTA 1500
Qy 559 Thr-----LeuAsnIleMetGlyaspAsp 566
Db 1501 TCCCGTGAAGCAGATTATGATTTTCCATGACAGACTGATTAACAGCTACCTAGAAC 1560
Qy 567 Tyrglu-----SerCysIleArgaspProGly 575
Db 1561 AATGAATTAAGAAATATGATTAAGAACAGCTCCGAGCAATTTGTAACAGAGATCTCTTA 1620
Qy 576 TyrgIysIysleuGlnMetLeuValIysHisIleGluSerGlyIleValleuGluGluasp 595
Db 1621 TCTGAA-----ATCAGTGAAGCA 1638
Qy 596 GluGlnArgHisValTPraspMetTPraspArgTyrg-----IleGlnIysGlnIuPro 612
Db 1639 GAGAAAGATTTTCTGTGAGCAGACACACATTTGTGTAATCTGACCCGAAATTTTACC 1698
Qy 613 AspLeuLeuIleValleuSerGluLeuAlaPheValTPraspArgGluAsnPheSer 632
Db 1699 AATATGCT-----CTGCTGTTAATGAAGACTGACAGATGAATGACT 1743
Qy 633 GluLeuTyrgValMetLeuGluIysTPraspProProSerValAlaAlaIleuThrIleu 652
Db 1744 CAGATGACTGCTGTGTAAGATTTGGCTCCAAATCAAGCTGAACAGGCTATGAGCT 1803
Qy 653 LeuGlyIysArgCysThrAspArgValIleArgIysPheAlaValIysleuAsnGlu 672
Db 1804 CTGAGCTCAATTACCAGATCTATGCTGAGGTTTGTGCTTGGCTGCTTACAAAAA 1863
Qy 673 GluLeuSerProValThrPheHisleuPheIleuProleuIleGlnAlaLeuIysTyrg 692
Db 1864 TATTTAACAGATGACAACTTTCTCAGTACCTTAATTCAGCTGATGACTATAAATAT 1923
Qy 693 GluProArgAlaGlnSerGluValGlyMetMetLeuLeuThrArgAlaLeuCysaspTyrg 712
Db 1924 GAACAGTATTTGATTAACCTGCTGTGAGATTTTATCTCAAAAAGCGTTAACTATCA 1983
Qy 713 ArgIleGlyHisArgLeuPheThrPheLeuArgAlaGluIleAlaArgLeuArgaspCys 732
Db 1984 AGATGGCTGACTTTTCTTTGGCATTTAAATCTGAGATGCAC----- 2028
Qy 733 AspLeuIysSerGluGlyTyrgArgArgIleSerLeuMetGluAlaTyrgLeuArgGly 752
Db 2029 -----AATTAACAAGTATGACAGAGTTTGGCTGCTTTGAGATCTATGCGCTGCA 2082
Qy 753 AsnGluGluHisIleIysIleIleThrArgGlnValaspMetValaspGluLeuThrArg 772
Db 2083 TGTGGATGATATCTGAAGCACTTAATAGCGCAAGTTGAGGCTATGAAAAGCTCATTAAC 2142

773 ILeSerThrLeuValIleGlyMetProIlyAspValAlaThrMetLysLeuArgAspGlu 792
 2143 TTGACTGACATCTCCAAACAGAAAGAAAGAT---GAAACCAAAAGTA-----CAG 2193
 793 LeuArgSerIleSerHisLysMetGluAsnMetAsp----- 804
 2194 ATGAAGTTTATAGTGAACAAATGCGGCGACCAAGATTTTCATGATGATCTCCAGGCGCTTT 2253
 805 ---SerProLeuAspProValIlyThrLysLeuGlyGluMetIleIleAspLysAlaIleVal 823
 2254 CTGTCTCTTCAACCTGCTGCTCATGAGCTGAGAAATCTCAGGCTTGAGAGTGTGCAATT 2313
 824 LeuGlySerAlaLysArgProLeuMetLeuHisIleThrLysAsnLysAsnProLysSerAsp 843
 2314 ATGTTCTTCGAAAAGGCACTGTGTGATTTGGAGAACCCAGACATCATGTGCAAGA 2373
 844 LeuHisLeuProPheCysAlaMetIlePheLysAsnGlyAspAspLeuArgGlnAspPhe 863
 2374 TTACTCTTTCAGAACATGAGATCATCTTTAAATAATGGGAGATTTTACGCGCAAGATATG 2433
 864 LeuValLeuGlnValLeuGluValMetAspAsnIleThrLysAlaAlaAsnIleAspCys 883
 2434 CTAACTTCAACATTTGCGATTAATGGAATAATCTGCAAAATCAACAGCTTTGATCTT 2493
 884 CysLeuAsnProThrAlaValLeuProMetGlyGluMetIleGlyIleIleGluValAla 903
 2494 CGAATGTTACCTTATGAGATGTCTGTCAATCGGTGACTGTGGAGCTTATTCAGAGTGGT 2553
 904 ProAsnCysLysThrIlePheGluIleGlnValGlyThrGlyPheMetAsnThrAlaVal 923
 2554 AGAAATTTCTCACACATATATGACAGATTCAGTTAAAGAGCGCTGAAAGGTGACACTG--- 2610
 924 ArgSerIleAspProSerPheMetAsnLysThrIleArgLysGlnCysGlyIleGluAsp 943
 2611 ---CAGTTTAAAGCCACACACTTCATCTGCTGCTC----- 2643
 944 GluLysLysSerLysAspSerThrLysAsnProIleGluLysLysIleAspAsn 963
 2644 ---AAAGACAAAGAAACAAAGGGGAAAT--- 2667
 964 ThrGlnAlaMetLysLysThrPheGluSerValAspArgPheLeuTyrSerCysValGly 983
 2668 ---TATGATCGGCGCATGATGATTTGTTTACACAGATCATGATGCTGGA 2709
 984 TyrSerValAlaThrThrIleMetGlyIleLysAspArgHisSerAspAsnLeuMetLeu 1003
 2710 TATGTGTGTCACCTTATTTGGAAATGAGATCGTCAACAAATGATTAATCATGTGTT 2769
 1004 ThrGluAspGlyLysTyrValHisIleAspPheGlyHisIleLeuGlyHisIleGlyLysThr 1023
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 1024 LysLeuGlyIleGlnArgAspArgGlnProPheIleLeuThrGlnHisPheMetThrVal 1043
 2830 AAATTTGTTTAAACGAGAGCGCGCTGTTTGTTCACACAAGATTTCTTAATAGTG 2889
 1044 IleArgSerGlyLysSerValAspGlyAsnSerHisIleGluLeuGlnLysPheLysThrLeu 1063
 2890 ATTACTAAAGAGCCCAAGATGCAACAAAGCAAGAAATTTTGAAGGTTTACAGAGATG 2949
 1064 CysValGlnAlaIlyGluValMetThrAsnAsnArgAspLeuPheValSerLeuPheThr 1083
 2950 TGTTCAGAGGCTTATCTAGCTTATGCGGACGATGCCAATCTTTTATATAATCTTTTCTCA 3009
 1084 LeuMetLeuGlyMetGluLeuProGluLeuSerThrLysAlaAspLeuAspHisLeuLys 1103
 3010 ATGATGCTTGCTGAGATGCAAGACTGCAATCTTTTATGATATGATTCATACATTCGA 3069
 1104 LysThrLeuPheCysAsnGlyLysLysGluGluAlaArgLysPhePheHisIleGlyIle 1123
 3070 AAGACCTTAGCTTATGAT---AAACCTGACAAAGGCTTTGAGATTTTCAATGAAACA 3126
 1124 TyrGluGlnAlaPheAsnGlySerThrSerThrLysThrAsnThrLeuPheHisAlaVal 1143

3127 ATGATGATGACACACATGATGCTGCGACACAAATAATGATGATGATCTTCACACAAAT 3186
 1144 LysHisTyr 1146
 3187 AAGCAGCAT 3195
 Db 3187 AAGCAGCAT 3195
 RESULT 5
 US-08-162-081B-34
 ; Sequence 34, Application US/08162081B
 ; Patent No. 5824492
 ; GENERAL INFORMATION:
 ; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
 ; APPLICANT: Balaj, Waterfield, Michael Derek; Parker, Peter
 ; APPLICANT: Joseph, Oren; Masayuki; Panayotou, George; Volinia,
 ; APPLICANT: Stefano; Gout, Ivan Tarasovitch
 ; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
 ; NUMBER OF SEQUENCES: 50
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Felfe & Lynch
 ; STREET: 805 Third Avenue
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10022
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: Wordperfect
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/162,081B
 ; FILING DATE: February 7, 1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/GB93/00761
 ; FILING DATE: 13 April 1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Pasqualini, Patricia A.
 ; REGISTRATION NUMBER: 34,894
 ; REFERENCE/DOCKET NUMBER: LUD 5256
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 688-9200
 ; TELEFAX: (212) 838-3884
 ; INFORMATION FOR SEQ ID NO: 34:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3240 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-162-081B-34
 Alignment Scores:
 Pred. No.: 7,16e-119 Length: 3240
 Score: 1082.00 Matches: 309
 Percent Similarity: 47.13% Conservative: 225
 Best Local Similarity: 27.27% Mismatches: 437
 Query Match: 17.90% Indels: 162
 DB: 1 Gaps: 39
 US-08-908-453-1 (1-1146) x US-08-162-081B-34 (1-3240)
 70 GluIleLysLeuSerAspPheLysHisIleGluLeuPheGluLeuIleAlaProMetLysTrp 89
 115 GAGGCTACATATGTAACATTAAGATGACATGAACTTATA-----GAAGCAAGAAATAAC 168
 90 GlyThrTyrSerValLysProGlnAsp-----TyrValPheArgGlnLeuAsnAsnHe 107
 169 CCTTCACATCAACTTTCGAAGATGATCTTTCATATTTGTAAGTGTTAACCAAGAA 228
 108 GlyIleGluValIlePheAsnAspAspGlnProLeuSerLysLeuGluLeuHisGly 127

Db 229 GCAGAAAGGAGAAATTTTGTATGAAACAGACGACTTGTGATCTCGGCTTTTCA 288
 Qy 128 ThrPheProMetLeuPheLeuTyrglnProAspGlyIleAsnArgAspLeuMet 147
 Db 289 -----CCATTTTAAAGTAATGTAACAGTAGGACGACGTAAGAAAAGATCCCTCAT 342
 Qy 148 SerAspIleSerHisCysLeuGlyTyrserLeuAspLeuGluGluSerLeuAspGlu 167
 Db 343 CGAGAAATTTGGTTTCTTCATCGCATCCAGCTGCGAAATTTGATATGGTTAAAGTCC 402
 Qy 168 GluLeuArgGlnPheArgIleSerLeuTrpAlaArgThrLysLysThrCysLeuThrArg 187
 Db 403 GAAGTACGAGACTTCGAGAGAAATATTCTTAATGTTGTAAGAAGCTGTGATCTTAG 462
 Qy 188 GlyLeu-----GluGlyThrSerHisTyrglnAlaPheProGluGluGlnTyrcys 204
 Db 463 GATCTTAATTCACCTCATAGTAGAGCAATGTATGCTATCCG-----CCACATGTAGAA 516
 Qy 205 ValGlyGluSerCysProLysAspLeuGluSerLysValLysValAlaLysLeuSerTyrc 224
 Db 517 TCTTACCCAGAGCTGCCAAGCACATATATATTAATTTGATAGAGCCAAATA---ATA 573
 Qy 225 GlnMetPheTrp-----ArgLysArgLysAlaGluIle 235
 Db 574 GTGGTATTTGGGTAAATAGTTTCTCCAAATTAATGACAGACAGATATCTGTGAATAATC 633
 Qy 236 AsnGlyValCys-----GluLysMetMetLysIleGlnIleGluPheAsnProAsnGlu 253
 Db 634 AACCATGACTGTGTGCCAGAACAAATTAATGCTGAAGCAATACAG-----AAAAA 684
 Qy 254 ThrProLysSerLeuHisThrPheLeuTyrglnMetArgLysLeuAspValTyrcys 273
 Db 685 ACTAGAAAGTATGTGCTATCATCT-----GAACATTAATAACTGTGTGTTTAGAA 735
 Qy 274 ThrAspAspProAlaAspGluGlyTrpPheLeuGlnLeuAlaGlyArgThrThrPheVal 293
 Db 736 TATCAGGCGAAG-----TACATTTTAAAGTGTGTGATGATGATGATGATCTTC 783
 Qy 294 ThrAsnProAspValLysLeuThrSerTyrglnAspGlyValArgSerGluLeuGluSerTyrc 313
 Db 784 CTAGAA---AAATATCTCTGAGTACGTAAATAGTATTAAGAAAGCTGTAAATGCTTGG 840
 Qy 314 ArgCysProGlyPhe---ValValArgArgGlnSerLeuValLeuLysAspTyrcysArg 332
 Db 841 AGAGTCCCAATTTGAAGATGATGATGCTAAAGAAAGCTTTAT----- 882
 Qy 333 ProLysProLeuTyrglnProHisTyrglnAlaArgAlaHisGluArgLysLeuAlaLeuAsp 352
 Db 883 -----TCTCACTGCGCAATGAGAC 900
 Qy 353 ValLeuSerValSerIleAspSerThrProLysGlnSerLysAsnSerAspMetValMet 372
 Db 901 TGTTTTACATG-----CCATCTTATTCACAGCGACTTTCACAGCTTACA 945
 Qy 373 ThrAspPheArgProThrAlaSerLeuLysGlnValSerLeuTrpAspLeuAspAlaAsn 392
 Db 946 CCATATATGAATGAGAAACATCTACAAA-----TCCCTTTGGGTTTAATATAGACA 999
 Qy 393 LeuMetIleArg-----ProValAsnIleSerGlyPheAspPhe 405
 Db 1000 CTCAGATATAAAATCTTGTGCAACCTATGTGAATGAATTAATTTGAGACATTGAC--- 1056
 Qy 406 ProAlaAspValAspMetTyrglnValArgIleGluPheSerValTyrglnGlyThrLeuThr 425
 Db 1057 -----AAGATTATATGTTGAAACA-----GATATCTACATGAGAGAGAACCC 1098
 Qy 426 LeuAlaSerLys---SerThrThrLysValAsnAlaGlnPheAlaLysTrpAsnLysGlu 444
 Db 1099 TTAATGACAAATGTGAACACTCAAAAGATACCTTGTCCAAATCCAGCTGGAAT---GAA 1155
 Qy 445 MetTyThrPheAspLeuTyrcysMetLysAspMetProProSerAla-----ValLeuSer 462
 Db 1156 TGAGCTGAATATGATATATACATTTCTGATCTTCTCGTGTGCTGCTGCACTTTCCTTTC 1215

Qy 463 IleArgValLeuTyrglnLysValLysLeuLysSerGluGluPheGluValGlyTyrglnVal 482
 Db 1216 ATTGCTCTGTAAAGCGAAAGGGCTCTTAAGAGGAACCTGTCCATTTGGCATTTGGGA 1275
 Qy 483 AsnMetSerLeuThrAspTrpArgAspGluLeuArgGlnGlyGlnPheLeuPheHisLeu 502
 Db 1276 AATATAACTGTTTGTATACACAGACACTAGATGTGGAAAAAGGCTTTGATGATCTT 1335
 Qy 503 TrpAlaProGluProThrAlaAsnArgSerArgIleGlyGluAsnGlyAlaArgIleGly 522
 Db 1336 TGG---CCAGTACCTCATGAGATTAGAAAGATTGTGCAACCTATTTGGTGT---ACTGGA 1389
 Qy 523 ThrAsn-----AlaAlaValThrIleGluIleSerSerTyrcylValArg 537
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 Qy 538 ValArgMetProSerGlnGlyGlnTyrglnThrTyrglnValLysHisArgSerThrTrpThr 557
 Db 1450 GTAAGTTCACAGATATGTCA-----GTGATTGAAGAGCATGCCAATGTGTCT 1497
 Qy 558 GluThr-----LeuAsnIleMetGlyAsp 565
 Db 1498 GTATCCCGAGAGCAGATTTAGCTATTCCACGAGACTGAGTAAACAGACTAGCTAGA 1557
 Qy 566 AspTyrglnSerCysIleArgAspProGlyTyrglnLysLeuGlnMetLeuValLysLys 585
 Db 1558 GACAAATGA-----TTAAGGAAATATGACAAAGAACCTCCAAAGCAATTTCTACACGA 1611
 Qy 586 HisGluSerGlyIleValLeuGluGluLysAspGluGlnArgHisValTrpMetTrpArgArg 605
 Db 1612 GATCCTCTCTGGAATACAGTACGAGCAG---GAGAAAGATTTCTTATGAGTACAGACAC 1668
 Qy 606 Tyr-----IleGlnLysGlnIleProAspLeuLeuIleValLeuSerGluLeuAla 622
 Db 1669 TATTGTGTAATCTATCCCGAAATTTCTACCCAAATGTCT-----CTGTCT 1713
 Qy 623 PheValTrpThrAspArgGluAsnAspSerGluLeuTyrglnValMetLeuGluLysTrpLys 642
 Db 1714 GTTAATAGGAATTTCTAGAGATGAAGTACCCAGATGTAATTTGCTGTGTAAGATGGCCT 1773
 Qy 643 ProProSerValAlaAlaAlaLeuThrLeuLeuGlyLysArgCysThrAspArgValIle 662
 Db 1774 CCAATCAAAACCTGAACAGCGATATGAGACTTGTGAGCTGAATTAACAGATCTTATGGT 1833
 Qy 663 ArgLysPheAlaValGluLysLeuAsnGluGlnLeuSerProValThrPheHisLeuPhe 682
 Db 1834 CGAGGTTTGTGCTGTGCGTGTGGAATAATTTTAACAGATGACAAACTTTCTCAGTAT 1893
 Qy 683 IleLeuProLeuIleGlnAlaLeuLysTyrglnProArgAlaGlnSerGluValGlyMet 702
 Db 1894 TTAATTCAGCTATGTAAGGCTCTTAATAATGAAACAATTTGGAATTAACCTGTGTTGAGA 1953
 Qy 703 MetLeuLeuThrArgAlaLeuCysAspTyrglnIleGlyHisArgLeuPheTrpLeuLeu 722
 Db 1954 TTTTATCGAAGAAAGCAATGACTATCAAGAGATTTGGCACTTTTCTTTTGGCATTTA 2013
 Qy 722 ArgAlaGluIleAlaArgLeuArgAspCysAspLeuLysSerGluGluTyrglnArgIle 742
 Db 2014 AAATCTGAGATGCAC-----AATTAACAGTTAGCCAGAGGTTT 2052
 Qy 743 SerLeuLeuMetGluAlaTyrglnArgGlyAsnGluGluHisIleLysIleIleThrArg 762
 Db 2053 GCGCTGCTTTTGAAGTCTTATGTGTGTCATGTGGATGTATTTGAAGCACTGTAATAG 2112
 Qy 763 GlnValAspMetValAspGluLeuThrArgIleSerThrLeuValLysGlyMetProLys 782
 Db 2113 CAAGTCAGGCAAGGAAAGCTCATTAATCAATGACATCTTCAACAGAGAGAGGAAG 2172
 Qy 783 AspValAlaThrMetLysLeuArgAspGluLeuArgSerIleSerHisLysMetGluAsn 802
 Db 2173 GAT---GAAACCAAAAGGTA-----CAGATGAAGTTTATGTTAGACCAATTAAGGCGCA 2223

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QY 803 MetAsp-----SerProLeuAspProValTyrIleu 813
Db 2224 CCAGATTCATGATGACCTCAGAGGCTTGCTGCTCTTAACCTGCTCATCACTA 2283
QY 814 GlyIleuMetIleIleAspIleValIleValIleuGlySerAlaIleArgProIleuMetIleu 833
Db 2284 GGAACCTCAGGCTTAAAGAGTGCAGAAATTAAGTCTTTCGCAAAAAGCCATGGCTGG 2343
QY 834 H1STPLYSAsnIleAsnProIleSerAspIleuH1sLeuProPheCysAlaMetIlePhe 853
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QY 854 LysAsnGlyAspAspLeuArgIleAspMetIleuValIleuGlnValIleuValMetAsp 873
Db 2404 AAAAATGGGGATGATTTACGCGCAAGATATGCTAACACTTCAATATTGCTATGTGA 2463
QY 874 AsnIleTPrIleValAlaAlaAsnIleAspCysIleAsnProTyrAlaValIleuProMet 893
Db 2464 AATATCTGGCAAAATCAAGGCTTGTATCTTGAATGTACCTTATGCTGTCTGCAATC 2523
QY 894 GlyIleuMetIleGlyIleIleGlnValIleProAsnCysIleTyrIlePheGlnIleGln 913
Db 2524 GGTGCTGTGTGGGCTTATTAAGGTGCGCAAAATTCACACTATTTATGCAAAATTCAG 2583
QY 914 ValGlyThrGlyPheMetAsnThrAlaValAlaSerIleAspProSerPheMetAsnIlys 933
Db 2584 TGCAGAGCGGCTTAAAGGTGCACTG-----CAGTTCAACAGCCACACTACATCAG 2637
QY 934 TrpIleArgIleGlnCysGlyIleGlnAspGlnIleIleValSerIleValAspSerThr 953
Db 2638 TGGCTC-----AAAACACAGAAC 2655
QY 954 LysAsnProIleGlnIleValSerIleAspAsnThrGlnAlaMetIleValSerIleGlnIle 973
Db 2656 AAAGAGAAAT-----TATCATGCAGCC 2679
QY 974 ValAspArgPheLeuTyrSerCysValGlyTyrSerValAlaIleThrTyrIleMetGlyIle 993
Db 2680 ATTGACCTGTTTACAGTTCATGCTGCTGATCTGCTGATGCTGCTGCTGCTGCTGCTG 2739
QY 994 LysAspArgIleSerAspAsnIleuMetIleuThrGlnAspGlyIleTyrValH1sIleAsp 1013
Db 2740 GGAGATCGTCACAAATGTAACATCTGGAAGACATGACCACTGTTTCATATAGAT 2799
QY 1014 PheGlyH1sIleLeuGlyH1sGlyIleThrIleValIleGlyIleGlnArgAspArgIlePro 1033
Db 2800 TTTGGACACTTTTGGATCACAAGAAATAATTTGTTATTAACGAAACGCTGCCA 2859
QY 1034 PheIleLeuThrGlnH1sPheMetThrValIleArgSerGlyIleSerValAspGlyAsn 1053
Db 2860 TTTGTTTGGACACAGATTTCTTATAGATTAAGGAGCCCAAGATGCAACAAG 2919
QY 1054 SerH1sGlnIleuGlnIlePheIleuThrIleuCysValGlnAlaIleGlnValMetIleTrpAsn 1073
Db 2920 ACAAGAGAAATTTGAGAGGTTTCAAGAGATGTGTTCAAGGCTTATCTGATTCAGCAG 2979
QY 1074 AsnArgAspLeuPheValSerIleuPheThrIleuMetIleuGlyIleuGlnIleuProIleu 1093
Db 2980 CATGCATCTCTTATTAATCTTTTCAATGATGCTGCTGCTGCAATGCAACAAC 3039
QY 1094 SerThrIleValAspLeuAspH1sIleuIleValIleuPheCysAsnGlyIleuSerIlys 1113
Db 3040 CAATCTTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3096
QY 1114 GlnGlnIleValAspIlePheAsnAspAspIleProIleuSerIleuGlnIleuH1sGly 1133
Db 3097 CAAGGCTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3156
QY 1134 ThrIleThrAsnIleuPheH1sAlaValIleuH1sIleu 1146
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US-08-780-872-34
; Sequence 34, Application US/08780872
; Patent No. 5846824
; GENERAL INFORMATION:
; APPLICANT: Hilee, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
; APPLICANT: Stefano; Gout, Ivan Tarasovitch
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; TITLE OR INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780, 872
; FILING DATE: 09-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/162,081
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: PCT/GB93/00761
; FILING DATE: 13 April 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: LOD 5256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-780-872-34
Alignment Scores:
Pred. No.: 7,166-119 Length: 3240
Score: 1082.00 Matches: 309
Percent Similarity: 47.13% Conservative: 225
Best Local Similarity: 27.27% Mismatches: 437
Query Match: 17.90% Indels: 162
DB: 2 Gaps: 39
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QY 90 GlyThrTyrSerValIleProGlnAsp-----TyrValPheArgIleuAsnAsnIle 107
Db 169 CCTCTCCATCAACTTCTTCAAGATGAACTTCTTACATTTTCGTAAGTGTACCCAGAA 228
QY 108 GlyIleuIleGlnValIlePheAsnAspAspIleProIleuSerIleuGlnIleuH1sGly 127
Db 229 GCAGAAAGGAAAGATTTTGTATGATGAAACAGACATTTGTGATCTTGGCTTTTCA 288
QY 128 ThrPheProMetIleuPheIleuTyrGlnIleProAspGlyIleAsnAspAspIleuMet 147
Db 289 -----CCATTTTAAAGTAATGAAACAGTACGCAACCGTGAAGAAAGATCTCAT 342

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QY 148 SerAspIleSerHisCysLeuGlyTyrSerLeuAspArgLeuGluGluSerLeuAspGlu 167
 Db 343 CGAAGAAATGGCTTTTGGCTATGCGCATGCCAGTGTGGCAATTGGATTGGTTAAAGATCCT 402
 QY 168 GluLeuArgGlnPheArgHisLeuThrAlaArgThrLeuLeuLeuThrCysLeuThrArg 187
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 QY 188 GlyLeu-----GluGlyThrSerHisTyrAlaPheProGluGlnGlyLeuCys 204
 Db 463 GATCTTAATTCACCTCATAGTAGAGCAATGATGTCTATCCG-----CCACATGAGAA 516
 QY 205 ValGlyGluSerCysProLeuAspLeuGluSerLeuValLeuAlaLeuLeuSerTyr 224
 Db 517 TCTTCAACGAGACTGCCAAGACATATATTAATATGATAGAGGCCAAATA--ATA 573
 QY 225 GlnMetPheTyr-----ArgLeuArgLeuAlaGluLeu 235
 Db 574 GTGGGATTTGGGTATAGTATTCTCCAAATTAATGACACAGAGATATCTGTGAATATC 633
 QY 236 AsnGlyValCys-----GluLeuMetMetLeuLeuGlnLeuPheAsnProAsnGlu 253
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 QY 254 ThrProLeuSerLeuLeuHisThrPheLeuTyrGluMetArgLeuLeuAspValTyrAsp 273
 Db 685 ACTAGAGATGTGTGCTATCATCT-----GAAACAATTAAACTGTGTGTTTGA 735
 QY 274 ThrAspAspProAlaAspGluGlyTyrPheLeuGlnLeuAlaGlyArgThrThrPheVal 293
 Db 736 TATCAGGGGCAAG-----TACATTTTAAAGTGTGTGAGATGATGATGAATCTTC 783
 QY 294 ThrAsnProAspValLeuLeuThrSerTyrAspGlyValArgSerGluLeuGluSerTyr 313
 Db 784 CTAGAA--AAATATCCTGTGAGTCAGTAAAGTATATTAAGAAAGCTGTATATGCTTGG 840
 QY 314 ArgCysProGlyPhe--ValValArgArgGlnSerLeuValLeuLeuAspTyrCysArg 332
 Db 841 AGGATGCCCAATTTGAAAGTATGATGCTTAAGAAAGCTTTAT----- 882
 QY 333 ProLeuProLeuTyrGluProHisTyrValArgAlaHisGluArgLeuAlaLeuAsp 352
 Db 883 -----TCTCACTGCCCAATGAGC 900
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 Db 901 TGTTTTACATG-----CCATCTTATTCAGAGCATTTCCACAGCTTACA 945
 QY 373 ThrAspPheArgProThrAlaSerLeuLeuGlnValSerLeuThrAspLeuAspAlaAsn 392
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 QY 426 LeuAlaSerLeu--SerThrThrLeuValAsnAlaGlnPheAlaLeuSerPheAsnGlu 444
 Db 1099 TTAATGCAAAATGTAACACTCAAAAGATACCTTTCCAAATCCCAAGCTGGAT---GAA 1155
 QY 445 MetTyrThrPheAspLeuTyrMetCysAspMetProProSerAla-----ValLeuSer 462
 Db 1156 TGGCTGAATTAATGATATATACATTCCTGATCTTCCTGTGCTGCTGCACTTTCCTTCC 1215
 QY 463 IleArgValLeuTyrGlyLeuValLeuLeuSerGluGluPheGluValGlyTyrPheVal 482
 Db 1216 ATTTGCTCTTAAAGCCGAAAGGCTTAAAGAGAACACTGTCCATTCGATGGAGGGA 1275
 QY 483 AsnMetSerLeuThrAspTyrArgArgGluLeuArgGlnGlyPheLeuPheHisLeu 502

Db 1276 AATATAACTGTTGATTATACACAGACACTAGATCTGGAAAGATGCTTGAATCTT 1335
 QY 503 TrpAlaProGluProThrAlaAsnArgSerArgIleGlyValAsnGlyAlaArgIleGly 522
 Db 1336 TGG--CCAGTACCTCATGATTAAGAAATTTGCTGAAACCTATATGGTGT--ACTGGA 1389
 QY 523 ThrAsn-----AlaAlaValThrIleGluIleSerSerTyrGlyValArg 537
 Db 1390 TCAAAATCCAAATTAAGAAATCTCATGCTTGAAGTTGGAGTTTGACTGTGACAGCTG 1449
 QY 538 ValArgMetProSerGlnGlyGlnTyrThrTyrLeuValLeuHisArgSerThrTrpThr 557
 Db 1450 GTAAGTCCCAAGATATGCA-----GTGATGAAGACAGACATGGCATGGTCT 1497
 QY 558 GluThr-----LeuAsnIleMetCysAsp 565
 Db 1498 GTATCCGAGAGCAGATTTAGCTATTCCACGAGAGACTGATACAGACTAGCTAGA 1557
 QY 566 AspTyrGluSerCysIleArgAspProGlyTyrTyrLeuLeuGlnMetLeuValLeuLeu 585
 Db 1558 GACAAATGAA-----TTAAGGAAATATGACAAAGACAGCTCAAAAGCAATTTCTACAGA 1611
 QY 586 HisGluSerGlyIleValLeuGluGluAspGluGlnArgHisValTrpMetTrpArgArg 605
 Db 1612 GATCCTCTCTGAAATCAGTCAGCAG--GAGAAAGATTTTCTATGAGTGCACAGACAC 1668
 QY 606 Tyr-----IleGlnLeuGlnLeuProAspLeuLeuIleValLeuSerGluLeuAla 622
 Db 1669 TATTCGTAACTATCCCGAAATTTCTACCAATTTGCTT-----GTGCT 1713
 QY 623 PheValTrpThrAspArgGluAsnAspSerGluLeuTyrValMetLeuGluTyrTrpLeu 642
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 QY 643 ProProSerValAlaAlaLeuThrLeuLeuGluGlyLeuArgCysThrAspArgValIle 662
 Db 1774 CCAATCAACCTGAAACAGAGCTATGAGACTTGTGACGTAAATTAACAGATCCATGTGT 1833
 QY 663 ArgGlyPheAlaValGluLeuLeuAsnGluGlnLeuSerProValThrPheHisLeuPhe 682
 Db 1834 CGAGGTTTGTCTGTGCTGCTGCTGGAATAATTTTAACAGATGACAACTTTCTCAGAT 1893
 QY 683 IleLeuProLeuIleGlnAlaLeuLeuTyrGluProArgAlaGlnSerGluValGluMet 702
 Db 1894 TTAATTCAGCTAGTACAGCTCTTAATAATGAAACAATTTTGGATTAACCTGCTGTGAGA 1953
 QY 703 MetLeuLeuThrArgAlaLeuCysAspTyrArgIleGlyHisArgLeuPheTrpLeuLeu 722
 Db 1954 TTTTATCTGAAGAAAGCATGATGATCAAAAGATTTGGCACTTTTCTTTGGCATTTA 2013
 QY 723 ArgAlaGluIleAlaArgLeuArgAspCysAspLeuLeuSerGluGluTyrArgArgIle 742
 Db 2014 AATCTGAGATGCAC-----AATTAACAGTTAGCCAGAGGTTT 2052
 QY 743 SerLeuLeuMetGluAlaTyrLeuArgGlyAsnGluGlnHisIleLeuIleLeuThrArg 762
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 Db 2113 CAAGTCGAGCAATGAGAAAGCTCATTAACCTAGCATCTCAAAACAGAGAGAGAAAG 2172
 QY 783 AspValAlaThrMetLeuLeuArgAspGluLeuArgSerIleSerHisLeuMetGluAsn 802
 Db 2173 GAT--GAAACCAAAAGGTA-----CAGATGAAGTTTATTGTTGAGCAAAATGAGCGCA 2223
 QY 803 MetAsp-----SerProLeuAspProValTyrTyrLeu 813
 Db 2224 CCAAGATTTATGAGATGCCCTTAAGGCTTGTCTCTCTTAACCTGCTCATCACTA 2283
 QY 814 GlyIleMetIleIleAspLeuAlaIleValLeuGlySerAlaLeuArgProLeuMetLeu 833

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Db      2284 GGAAACCTCAGGCTTAAGAGTGCAGATTATGCTTCGCAAAAAAGCCACTGCTTG 2343
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      2344 AATTGGAGAACCCAGACATCATGTCAGAGTTACTGTTCAAGAACATAGATCATCTTT 2403
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      2404 AAAAATGGGGATGATTACGGCAAGATATGTAACCTCAATTATTCGTTATGGA 2463
Qy      874 AsnIleTyrPlyAspAlaAlaAsnIleAspCysSLeuAsnProTyrAlaValLeuProMet 893
      2464 AATATCTGGCAAAATCAAGGCTTCATCTTCGAATGTATTCATGTTGTTGTCGAATC 2523
Qy      894 GlyGluMetIleGlyIleIleGluValValProAsnCysLysThrIlePheGluIleGln 913
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Qy      914 ValGlyThrGlyPheMetAsnThrAlaValArgSerIleAspProSerPheMetAsnLys 933
      2584 TCGAAAGGGGCTTGAAGGTGCACG-----CAGTTCAACAGCCACACTACATCAG 2637
Qy      934 TrpIleAspGlyGlnCysGlyIleGluAspGlyLysLysSerLysLysAspSerThr 953
      2638 TGGCTC-----AAAACAAGAAC 2655
Qy      954 LysAsnProIleGlyLysLysIleAspAsnThrGlnAlaMetLysLysTyrPheGluSer 973
      2656 AAGAGGAATAT-----TATATGACGACC 2679
Qy      974 ValAspArgPheLeuTyrSerCysValGlyTyrSerValAlaThrTyrIleMetGlyIle 993
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Qy      994 LysAspArgHisSerAspAsnLeuMetLeuThrGluAspGlyLysTyrValHisIleAsp 1013
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Qy      1014 PheGlyHisIleLeuGlyHisGlyLysThrLysLeuGlyIleGluAspArgGlnPro 1033
      2800 TTGGACACCTTTTGGATCACAAGAAAGAAATTTGTTATTAACGAGAACGTTGCCA 2859
Qy      1034 PheIleLeuThrGlnHisPheMetThrValIleArgSerGlyLysSerValAspGlyAsn 1053
      2860 TTTGTTTGGACACAGAGATTCTTATATAGATTAAGTAAGACCCCAAGATGACCAAG 2919
Qy      1054 SerHisGluLeuGlnLysPheLysThrLeuCysValGluAlaTyrGluValMetTyrAsn 1073
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Qy      1094 SerThrLysAlaAspLeuAspHisLeuLysLysThrLeuPheCysAsnLysLysLys 1113
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Qy      1114 GluGluAlaArgLysPhePheAlaGlyIleTyrGluGluAlaPheAsnGlySerTyrSer 1133
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```

APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
APPLICANT: Stefano; Gout, Ivan Tarasovitch
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
TITLE OF INVENTION: THEIR PREPARATION AND USE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,957
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/780,872
FILING DATE: 09-JAN-1997
APPLICATION NUMBER: 08/162,081
FILING DATE: February 7, 1994
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5256
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 3240 base pairs
TYPE: nucleic acid
STRANDNESS: single
TOPOLOGY: linear
US-09-085-957-34
Alignment Scores:
Pred. No.: 7,166-119 Length: 3240
Score: 1082.00 Matches: 309
Percent Similarity: 47.13% Conservative: 225
Best Local Similarity: 27.27% Mismatches: 437
Query Match: 17.90% Indels: 162
DB: 4 Gaps: 39
US-08-908-453-1 (1-1146) x US-09-085-957-34 (1-3240)
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Qy      90 GlyThrTyrSerValLysProGlnAsp-----TyrValPheArgGlnLeuAsnAsnPhe 107
      169 CCTCTCATCAACTCTTCAAGATGAATCTTCTTACATTTTCGTAAAGTTTACCCAGAA 228
Qy      108 GlyGluIleGluValIlePheAsnAspAspGlnProLeuSerLysLeuGluLeuHisGly 127
      229 GCAGAAAGGAGAAATTTTGTGATGAACAAGACACTTGTGATCTTCGGCTTTTTCAA 288
Qy      128 ThrPheProMetLeuPheLeuTyrGlnProAspGlyIleAsnArgAspLysGluLeuMet 147
      289 -----CATTTTAAAGTAAATGACACGAGAGCAACCGGAAGAAAGAAATCCTCAAT 342
Qy      148 SerAspIleSerHisCysLeuGlyTyrSerLeuAspLysLysGluGlnSerLeuAspGlu 167
      343 CGAGAAATTTGTTTGTCTATCGGCAATGCCAGTGTGCGCAATTTGATGATGATTAAGATCCT 402

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Qy 894 GlyLeuMetIleGlyIleIleGluValValProAsnCysLysTyrIlePheGluIleGln 913
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Qy 994 LysAspArgHisSerAspAsnLeuMetLeuThrGluAspGlyLysTyrValHisIleAsp 1013
Db 2740 GGAAGATCGTCACAAATGATGAATCATGCGTGAAGAGATGACAGCACTGTTTCAATTAAGT 2799
Qy 1014 PheGlyHisIleLeuGlyHisGlyLysThrLysLysGlyIleGlnArgAspArgGlnPro 1033
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Db 3040 CAATCTTTTGTATGATGATTCATGATCAATTCGAAAGACCTTACCTTAACTGAGT 3096
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Qy 1134 ThrLysThrAsnTrrLeuPheHisIleValLysHisTyr 1146
Db 3157 ACAAATAATGATGATGATCTTCCACACAATTAATAACAGCAT 3195

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RESULT 8

US-08-162-081B-32

Sequence 32, Application US/08162081B

Patent No. 5824492

GENERAL INFORMATION:

APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu

APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter

APPLICANT: Joseph, Otsu; Masayuki; Panayotou, George; Volinia,

APPLICANT: Stefano; Gout, Ivan; Tarasovitch

TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,

TITLE OF INVENTION: THEIR PREPARATION AND USE

```

NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSER: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,081B
FILING DATE: February 7, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5256
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-3884
TELEFAX: (212) 688-9200
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 3412 base pairs
TYPE: nucleic acid
STRANDEDNESS: single or double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3204
OTHER INFORMATION: /standard_name="CDS"
US-08-162-081B-32
Alignment Scores:
Pred. No.: 1.8e-118 Length: 3412
Score: 1079.00 Matches: 308
Percent Similarity: 47.13% Conservative: 226
Best Local Similarity: 27.18% Mismatches: 437
Query Match: 17.85% Indels: 162
Gaps: 39
US-08-908-453-1 (1-1146) x US-08-162-081B-32 (1-3412)
Qy 70 GluileLysLeuSerAspPheLysIleGlnLeuPheGluLeuIleAlaProMetLysTrr 89
Db 115 GAGGCTACATTAAGTACTATTAAGCATGACATTAATAA-----GAAGCAAGAAATTC 168
Qy 90 GlyThrTyrSerValLysProGlnAsp-----TyrValPheArgGlnLeuAsnAsn 107
Db 169 CCTCTCCATCAACTCTTCAAGATGAATCTTCAATTTTGTGTAAGTTAGTTAAAGATCCT 228
Qy 108 GlyGluIleGluValIlePheAsnAspArgGlnProLeuSerLysLysGluLeuHisGly 127
Db 229 GCAGAAAGGAGAAATTTTGTGATGACAAACAGACGACTTGTGATCTTCGGCTTTTCA 288
Qy 128 ThrPheProMetLeuPheLeuTyrGlnProAspGlyIleAsnArgAspLysGluLeuMet 147
Db 289 -----CATTTTAAAGTAATTAAGTAAGCAAGTGAACCGTGAAGAAAGATTCCTCAAT 342
Qy 148 SerAspIleSerHisCysLeuGlyTyrSerLeuAspLysLysGluGluSerLeuAspGlu 167
Db 343 CGAGAAATTTGTTTGTGATGCGCATGCGCATGCGCAATTTGATGATGATTAAGATCCT 402
Qy 168 GluLeuArgGlnPheArgAlaSerLeuTrrAlaArgThrLysLysThrCysLeuThrArg 187
Db 403 GAAGTACAGAGACTTCGGAAGAAATTAATCTTAATGTTGTTAAAGAGAGCTGTGATCTTAG 462

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 QY 205 ValGlyGluSerCysProLysAspLeuGluSerLysValIleAlaIleLeuSerTyr 224
 DB 517 TCTTACCAGACGCTGCGAAGACACATATATATTAATGTAGATAGAGCCAAATA---ATA 573
 QY 225 GlnMetPheTrp-----ArgLysArgLysAlaGluIle 235
 DB 574 GTGGGATTTGGGTATAGTCTTCTCCAAATTAATGACMACAGAGATATCTGTGAATAAC 633
 QY 236 AenglyValCys-----GluLysMetMetLysIleGlnIleGluPheAsnProAsnGlu 253
 DB 634 AACCATGACTGTGTGCCAGACACAGTAATGCTGAAGCAATCAGG-----AAAAA 684
 QY 254 ThrProLysSerLeuLeuHisThrPheLeuTyrGluMetArgLysLeuAspValTyrAsp 273
 DB 685 ACTAGAAATGATGTGTCTATCATCT-----GAACATTAATAACTGTGTGTTTAGAA 735
 QY 274 ThrAspAspProAlaAspGluGlyTyrPheLeuGlnLeuAlaGlyArgThrPheVal 293
 DB 736 TATCAGGGCAG-----TACATTTTAAAGTGTGTGATGTGATGAATAACTTC 783
 QY 294 ThrAsnProAspValLysLeuThrSerTyrAspGlyValArgSerGluLeuGluSerTyr 313
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 QY 314 ArgCysProGlyPhe---ValValArgArgGlnSerLeuValLeuLysAspTyrCysArg 332
 DB 841 AGGATGCCCAATTTGAAATGATGATGCTTAAGAAAGCCTTAT----- 882
 QY 333 ProLysProLeuTyrGluProHisTyrValArgAlaHisGluArgLysLeuAlaLeuAsp 352
 DB 883 -----TCTCACTGCCCAATGAGC 900
 QY 353 ValLeuSerValSerIleAspSerThrProLysGlnSerLysAsnSerAspMetValMet 372
 DB 901 TGTTTTACAAATG-----CCATCTTATTCAGACGCACTTCCACAGCTACA 945
 QY 373 ThrAspPheArgProThrAlaSerLeuLysGlnValSerLeuTyrAspLeuAspAlaAsn 392
 DB 946 CCATATATGAAATGAGAAACATCTACAAAA-----TCCCTTGGGTATTAATAATAGAGA 999
 QY 393 LeuMetIleArg-----ProValAsnIleSerGlyPheAspPhe 405
 DB 1000 CTCAGATTAATAATCTTGTGTGCAACCTACGTGAATCTAAATATTGAGACATTGAC--- 1056
 QY 406 ProAlaAspValAspMetTyrValArgIleGluPheSerValTyrValGlyThrLeuThr 425
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 QY 503 TrpAlaProGluProThrAlaAsnArgSerArgIleGlyGluAsnGlyAlaArgIleGly 522
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 Qy 1034 PheIleLeuThrGlnHisPheMetThrValIleArgSerGlyLysSerValAspGlyAsn 1053
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 RESULT 9
 US-08-780-872-32
 ; Sequence 32, Application US/08780872
 ; Patent No. 5846824
 ; GENERAL INFORMATION:
 ; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
 ; APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter
 ; APPLICANT: Joseph, Otsu, Masayuki; Panayotou, George; Volinia,
 ; APPLICANT: Stefano, Gout, Ivan Tarasovitch
 ; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
 ; TITLE OF INVENTION: THEIR PREPARATION AND USE
 ; NUMBER OF SEQUENCES: 50
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Felte & Lynch
 ; STREET: 805 Third Avenue

CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10022
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: Wordperfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/780, 872
 FILING DATE: 09-JAN-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/162, 081
 FILING DATE: February 7, 1994
 APPLICATION NUMBER: PCT/GB93/00761
 FILING DATE: 13 April 1993
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 REGISTRATION NUMBER: 34,894
 REFERENCE/DOCKET NUMBER: LUD 5256
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 TELEPHONE: (212) 688-9200
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 INFORMATION FOR SEO ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3412 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single or double
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..3204
 OTHER INFORMATION: /standard_name="CDS"
 US-08-780-872-32
 Alignment Scores:
 Pred. No.: 1.8e-118 Length: 3412
 Score: 1079.00 Matches: 308
 Percent Similarity: 47.13% Conservative: 226
 Best Local Similarity: 27.18% Mismatches: 437
 Query Match: 17.85% Indels: 162
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 US-08-908-453-1 (1-1146) x US-08-780-872-32 (1-3412)
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 Qy 333 ProLysProLeuTyrGluProIleThrIleValArgAlaIleGluArgLysLeuAlaLeuAsp 352
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 RESULT 10
 US-09-085-957-32
 ; Sequence 32, Application US/09085957
 ; GENERAL INFORMATION:
 ; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
 ; APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter
 ; APPLICANT: Joseph, Otsu, Masayuki; Panayotou, George; Volinia,
 ; APPLICANT: Stefano; Gout, Ivan; Tarasovitch
 ; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
 ; NUMBER OF SEQUENCES: 50
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSES: Felife & Lynch
 ; STREET: 805 Third Avenue
 ; CITY: New York
 ; STATE: New York

COUNTRY: USA
 ZIP: 10022
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: Wordperfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/085,957
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/780,872
 FILING DATE: 09-JAN-1997
 APPLICATION NUMBER: 08/162,081
 FILING DATE: February 7, 1994
 APPLICATION NUMBER: PCT/GB93/00761
 FILING DATE: 13 April 1993
 ATTORNEY/AGENT INFORMATION:
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 REFERENCE/DOCKET NUMBER: LOD 5256
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 TELEPHONE: (212) 688-9200
 TELEFAX: (212) 838-3884
 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3412 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single or double
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..3204
 OTHER INFORMATION: /standard_name="CDS"
 US-09-085-957-32
 Alignment Scores:
 Pred. No.: 1,86-118 Length: 3412
 Score: 1079.00 Matches: 308
 Percent Similarity: 47.13% Conservative: 226
 Best Local Similarity: 27.18% Mismatches: 437
 Query Match: 17.85% Indels: 162
 DB: 4 Gaps: 39
 US-08-908-453-1 (1-1146) x US-09-085-957-32 (1-3412)
 QY 70 Glullelyleuseraspheleuyslyshisgluleuphegluleulealaproketytrp 89
 Db 115 GAGGCTACATTAGTACTATTAAGCATGACTATTAA-----GAAGCAAGAAATATC 168
 QY 90 Glythrlyservalylserproglinsp-----tyrvalphearghlnleuasnbnphe 107
 Db 169 CCTCTCATCAACTCTTCAAGATGAATCTTCTTACATTTCTGTAAGTTTACCAAGNA 228
 QY 108 Glyglullegluvalillepheasnaspahpbnproleuserlysleugluilehnsigly 127
 Db 229 GCAGAAAGGAAAGATTTTGTGATGAACAGACGACTTGTGATCTTCGGCTTTTCA 288
 QY 128 Thrpheapmetleupheleutyrcinproahsghlylleasnargsplygluleumet 147
 Db 289 -----CAATTTTAAAGTATTAACACAGTACGCAACCGTGAAGAAAGATCTCAAT 342
 QY 148 Seraspilserhlseserleuglytyrserleuphlylsleugluileuserleuphly 167
 Db 343 CGAGAAATGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 402
 QY 168 Glueuarghlnphearghlseserleuphlylathrlyshlythrlyshlythrlyshlythr 187
 Db 403 GAAGTACAGACTTCGAGAAATATTTCTTAATGTTTGAAGAGAGAGAGAGAGAGAGAGAGAG 462
 QY 188 Glyleu-----Gluglythrserhstlyrvalapheproglugluileuglytrcys 204

Db 463 GATCTTAATACCTCATAGTAGAGCAATGTATGCTATCCG-----CCACATGTAGAA 516
Qy 205 ValGlyUserCysProIlyAspLeuGlySerIlyValIlyAlaIlyLeuSerIlyr 224
Db 517 TCTTACACGAGACCTGCAGAAACATATTAATAATGATAGAGGCCAAATA---ATA 573
Qy 225 GlMetPheTrp-----ArgIlyAspIlyAlaIlyLeu 235
Db 574 GTGGGATTTGGGTAACTGTTCTCCAAATAATGACAGACAGATATATCTGTGAAATTC 633
Qy 236 AsnGlyValCys-----GlyIlySerMetIlyLeuIlyGlnIlyPheAsnProAsnGln 253
Db 634 AACCATGACTGTGTGCAGAAACAGTAATGTGCAAGCAATCAGC-----AAAAA 684
Qy 254 ThrProIlySerLeuLeuHsThrPheLeuIlyrGlnMetArgIlyLeuAspValIlyrAsp 273
Db 685 ACTAGAAATGTGTGTATCATCT-----GAACAAATTAACCTGTGTGTTTAGAA 735
Qy 274 ThrAspAspProAlaAspGluGlyrPheLeuGlnLeuAlaGlyrArgThrPheVal 293
Db 736 TATTCAGGGCAAG-----TACATTTTAAAGTGTGTGATGTGATGATATCTTC 783
Qy 294 ThrAsnProAspValIlySerLeuThrSerIlyrAspGlyValIlyrSerGlnLeuGlySerIlyr 313
Db 784 CTAGAA---AAATATCCTCTGAGTCACTAAGTATATAGAAAGCTGTATATGCTTGGG 840
Qy 314 ArgCysProGlyPhe---ValValIlyArgGlnSerLeuValIlyLeuIlyAspIlyrCysArg 332
Db 841 AGCATGCCCAATTTGAGATGATGTGCTAAAGAAAGCCCTTAT----- 882
Qy 333 ProIlyrProLeuIlyrGlnProHsIlyrValIlyrAlaHsIlyrGlnIlyrLeuAlaLeuAsp 352
Db 883 -----TCTCAACTGCCCAATGAGC 900
Qy 353 ValLeuSerValSerIlyAspSerThrProIlyrGlnSerIlyrAsnSerAspMetValMet 372
Db 901 TGTTTTACATG-----CCATCTTATTCAGACGCAATTCACAGCTTACA 945
Qy 373 ThrAspPheArgProThrAlaSerLeuIlyGlnValSerLeuIlyrAspLeuAspAlaAsn 392
Db 946 CCATATATGATGAGAGAAACATCTACAAA-----TCCCTTGGGTTTAAATAGACGA 999
Qy 393 LeuMetIlyArg-----ProValAsnIlySerGlyPheAspPhe 405
Db 1000 CTCAGAAATAAAATTTCTTGTGCAACCTACGTGATCTAAATTTTGACAACTTGC--- 1056
Qy 406 ProAlaAspValAspMetIlyrValIlyrGlnPheSerValIlyrValIlyrLeuThr 425
Db 1057 -----AAGATTATATGTTGAAACA-----GGTATCTACATGAGAGAAACCC 1098
Qy 426 LeuAlaSerIlyr-----SerThrIlyrValAsnAlaGlnPheAlaIlyrTrpAsnIlyrGln 444
Db 1099 TTATGTGACATGTGACACTCAAAAGATACCTTGTTCATCCACAGGTGAT---GAA 1155
Qy 445 MetIlyrThrPheAspLeuIlyrMetIlyrAspMetProProSerAla-----ValLeuSer 462
Db 1156 TGGCTGAATTTATATATATATATATCTCTGATCTTCTCTGCTGCTGCTGATGCTCTTTC 1215
Qy 463 IleArgValLeuIlyrGlyIlyrValIlyrLeuIlyrSerGlnIlyrPheGlnValIlyrVal 482
Db 1216 ATTTCCTGTGTAAAGCGCGAAAGGTGCTAAAGAGAAACACTGTCATGTCATGAGGAGA 1275
Qy 483 AsnMetSerLeuThrAspTrpArgAspGlnLeuArgGlnIlyrGlnPheLeuPheHsIleu 502
Db 1276 AATATAAAGCTTGTTAATTAACACAGACACTTAGTATCTGAAAGAAAGCTTGAATCTT 1335
Qy 503 TrpAlaProGlnProThrAlaAsnArgSerArgIlyrGlyIlyrAsnGlyAlaArgIlyrGly 522
Db 1336 TGG---CCAGTACTCATGATTAGAAGATTTGCTGAACCTATGTGT---ACTGGA 1389
Qy 523 ThrAsn-----AlaAlaValThrIleGlnIlyrSerSerIlyrGlyIlyrArg 537
Db 1390 TCAAAATCCAAATTAAGAAACTCATGCTTAGAGTTGAGTTTGACTGTTCACACAGTGTG 1449

Qy 538 ValArgMetProSerGlnIlyrGlnIlyrThrIlyrLeuValIlyrHsIlyrSerThrTrpThr 557
Db 1450 GTAAGGTTCCAGATATGTCA-----GTGATTGAAGACATGCCAATTTGGTCT 1497
Qy 558 GluThr-----LeuAsnIlyrMetClyAsp 565
Db 1498 GTATCCGAGAAAGACAGATTTAGCTATTCACAGCAGAGACTGATPACAGACTAGCTAGA 1557
Qy 566 AspIlyrGlySerCysIlyrArgAspProGlyIlyrIlyrIlyrLeuGlnMetLeuValIlyrIlyr 585
Db 1558 GACAAATGAA-----TTAAGGAAATGACAAAGAACGCTCAAGCAATTTCTACACGA 1611
Qy 586 HsGlySerGlyIlyrValLeuGlnIlyrAspGlnIlyrGlnIlyrHsIlyrValTrpMetTrpArgArg 605
Db 1612 GATCTCTCTGTGAATACTGAGCG---GAGAAAGATTTTCTATGAGTACACAGACAC 1668
Qy 606 Tyr-----IleGlnIlyrGlnIlyrProAspLeuLeuIlyrValLeuSerGlnIlyrAla 622
Db 1669 TATTTGTATCTATCCCGAAATTTCTACCAATTTGCTT-----CTGTCT 1713
Qy 623 PheValIlyrThrAspArgGlnAsnPheSerGlnLeuIlyrValMetLeuGlnIlyrTrpIlyr 642
Db 1714 GTTAATGGAATTTCTAGAGATGAACTAGCCAGATGATTTGCTGTGTAAGATTGGCCT 1773
Qy 643 ProProSerValAlaAlaIlyrLeuThrIlyrLeuGlnIlyrIlyrArgCysThrAspArgValIlyr 662
Db 1774 CCATCAAAACCTGAAACAGGCTATGGAACCTTCTGACGCTATATCCAGATCTATGTGT 1833
Qy 1774 ArgIlyrPheAlaValIlyrIlyrLeuAsnGlnIlyrLeuSerProValIlyrPheHsIlyrPhe 682
Db 1834 CGAGGTTTGTGCTTGGTGGTGAAGAAATATTAACAGATGACAAACTTCTCAGAT 1893
Qy 683 IleLeuProLeuIlyrGlnAlaLeuIlyrIlyrGlnProAlaGlnIlyrSerGlnValIlyrMet 702
Db 1894 TTAATTCAGCTAGTACAGCTCCTAAATAATGAAACATTTGGATTAACCTTGTGTGAGA 1953
Qy 703 MetLeuLeuThrArgAlaLeuCysAspIlyrArgIlyrGlnIlyrHsIlyrArgLeuPheTrpLeu 722
Db 1954 TTTTACGTAGAAAGCAATTTGACTATCAAAAGATTTGGCACTTTTCTTTGGCATTTA 2013
Qy 723 ArgAlaGlnIlyrLeuAlaArgLeuArgAspCysAspLeuIlyrSerGlnIlyrArgArgIlyr 742
Db 2014 AATCTGATGATCAC-----AATTAACAGTTAGCCAGAGGTT 2052
Qy 743 SerLeuLeuMetGlnAlaIlyrLeuArgIlyrAsnGlnIlyrHsIlyrIlyrLeuThrArg 762
Db 2053 GGCCTGCTTTTGGAGTCTATTTGTGTCATGTGATGTGATTTTGAACACCTGAAATAGG 2112
Qy 763 GlnValAspMetValAspGlnLeuThrArgIlyrIlyrSerThrIlyrLeuValIlyrGlyMetProIlyr 782
Db 2113 CAAGTCGAGCAATGAAAGCTCATTTAACTTATGCAATTTCTAAACAGAGAGAGAG 2172
Qy 783 AspValAlaThrMetIlyrLeuArgAspGlnLeuArgSerIlyrIlyrSerIlyrMetGlnAsn 802
Db 2173 GAT---GAAACCAAAAGSTA-----CAGATGAAGTTTGTAGAGCAATTAAGGCGGA 2223
Qy 803 MetAsp-----SerProLeuAspProValIlyrIlyrIlyr 813
Db 2224 CCAGATTTTCATGATGCCCTTACAGGCTTGTCTGTCTCTTAACCTGTCTATCACTA 2283
Qy 814 GlyIlyrMetIlyrAspIlyrAlaIlyrValIlyrLeuGlySerAlaIlyrArgProLeuMetLeu 833
Db 2284 GGAACCTCAGGCTTAAAGAGTGTGAAATTAATGTCTTCTGCAAAAGCCACTGTGCTTG 2343
Qy 834 HsIlyrIlyrAsnIlyrAsnProIlyrSerAspLeuHsIlyrProPheCysAlaMetIlyrPhe 853
Db 2344 AATGGGAGAACCCAGACATCATGTACAGAGTTACTGTTTCAAGACATAGATCATCTT 2403
Qy 854 IlyrAsnGlyAspAspLeuArgIlyrAsnMetLeuValLeuGlnValIlyrValMetAsp 873
Db 2404 AAAAATGGGAGATTTTACGGCAAGATATGTCTTAACATTCAATTAATTCGTATATGAA 2463

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Qy 874 AeniletrpLysalaalaenileapCysCysleuAsnProTyrAlaValleuProMet 893
Db 2464 AATATCTGGCAAAATCAAGGCTTGTGATCTTGAATGTACCTTATGTTGTCTGCAATC 2523
Qy 894 GlygluMetIleGlyIleIleGluValAlaProMetCysLeuThrIlePheGluIleGln 913
Db 2524 GGTGACTGTGGGACTTATTTGAGGCGGCAAAATCTCACATTTATGCAAAATTCAG 2583
Qy 914 ValGlyThrGlyPheMetAsnThrAlaValArgSerIleAspProSerPheMetAsnLys 933
Db 2584 TGCAAAAGGCGCTTGAAGGTGACATG-----CACTTCAACGCCACACACTACTCAG 2637
Qy 934 TrpIleArgLysGlnCysGlyIleGluAspGluLysLysSerLysLysAspSerThr 953
Db 2638 TGGCTC-----AAAGCAAGAAC 2655
Qy 954 LysAsnProIleGluLysLysIleAspAsnThrGlnAlaMetLysLysTyrPheGluSer 973
Db 2656 AAAGAGAAATA-----TATGATGCGAGCC 2679
Qy 974 ValAspArgPheLeuTyrSerCysValGlyTyrSerValAlaThrTyrIleMetGlyIle 993
Db 2680 ATTGACTGCTTTACACGTTTACATGCTGCTGATCTGTGATCTTACCTTCAATTTGGAAAT 2739
Qy 994 LysAspArgHisSerAspAsnLeuMetLeuThrGluAspGlyLysTyrValHisIleAsp 1013
Db 2740 GGAAGATCGTCACAAATAGTAACATCATGTGAAAGAACGATGCAACTGTTTCAATAGAT 2799
Qy 1014 PheGlyHisIleLeuGlyHisGlyLysThrLysLeuGlyIleGlnArgAspArgGlnPro 1033
Db 2800 TTTGGACACTTTTGGATGATCAAGAAAGAAATTTGGTTAATAAACGAAACGTGTGCCA 2859
Qy 1034 PheIleLeuThrGlnHisPheMetThrValIleArgSerGlyLysSerValAspGlyAsn 1053
Db 2860 TTTGTTTGACACAGGATTTCTTAATAGATTAGTAAGAGAGCCCAAGATGCACAAAG 2919
Qy 1054 SerHisGluLeuGlnLysPheLysThrLeuCysValGluAlaTyrGluValMetTrpAsn 1073
Db 2920 ACAAGAGAAATTTGAGAGGTTTCAAGGATGTTTCAAGGCTTATCTACTTCTTGACAG 2979
Qy 1074 AsnArgAspLeuPheValSerLeuPheThrLeuMetLeuGlyMetGluLeuProGluLeu 1093
Db 2980 CATGCCAATCTCTCATAAATCTTTCTCAATGATGCTTGGCTCGAATGCCAGAACTA 3039
Qy 1094 SerThrLysAlaAspLeuAspHisLeuLysThrLeuPheCysAsnGlyLysSerLys 1113
Db 3040 CAATCTTTTGATGACATTCATGATCAATCGAAAGACCCCTTAGAT--AAACTGAG 3096
Qy 1114 GluGluAlaArgLysPhePheAlaGlyIleTyrGluGluAlaPheAsnGlySerTrpSer 1133
Db 3097 CAAGAGCGCTTGGAGATTTCTATGAACAATGAATGATGCACATCATGTGGCTGGACA 3156
Qy 1134 ThrLysThrAsnTrpLeuPheHisAlaValLysHisTyr 1146
Db 3157 ACAAAAATGATGATGATCTTCCACACAAATTAACAGCAT 3195

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RESULT 11

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US-08-916-917-3
Sequence 3, Application US/08916917
Patent No. 5856132
GENERAL INFORMATION:
APPLICANT: Stephens, Len
APPLICANT: Phillip Thomas
APPLICANT: Braselmann, Sylvia
TITLE OF INVENTION: G-BETA-GAMMA REGULATED
TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSER: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA

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; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916,917
; FILING DATE: 15-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/672,211
; FILING DATE: 27-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Abrams, Samuel B
; REGISTRATION NUMBER: 30,605
; REFERENCE/DOCKET NUMBER: 8549-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3808 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-916-917-3

Alignment Scores:
Pred. No.: 1,83e-113 Length: 3808
Score: 1038.00 Matches: 316
Percent Similarity: 46.96% Conservative: 224
Best Local Similarity: 27.48% Mismatches: 400
Query Match: 17.17% Indels: 210
DB: Gaps: 46

US-08-908-453-1 (1-1146) x US-08-916-917-3 (1-3808)
Qy 68 SerLeuGluIleLysLeuSer--AspPheLysHisGlnLeu-----PheGlu 82
Db 330 GCGCTGGAGACGAGGCTTCTTGGGACTTCAACCGGTTCCGCCGCCACACTTCCCTC 379
Qy 83 LeuIleAlaProMetLysTrpGlyThrTyrSerValLysProGlnAspTrpValPheArg 102
Db 380 CTGGCTTCCAGAAAGAGGGAGTGTACGAGATCTATGACAAAGTACAGAGTGTGCGAG 439
Qy 103 GlnLeuAsnAsnPheGlyGluIleGluValIlePheAsnAspAspGlnProLeuSerLys 122
Db 440 ACCCTGAGATCGCTCGCTACGAGAGGTGTGACACCGAGCCCGGCGCATTCACAGT 499
Qy 440 ACCCTGAGATCGCTCGCTACGAGAGGTGTGACACCGAGCCCGGCGCATTCACAGT 499
Qy 123 LeuGluLeuHisGlyThrPheProMetLeuPheLeuTyrGlnProAspGlyIleAsnArg 142
Db 500 GTCCAGCGGCA GCGCCCTCGAGAGAGACATTGGCTTCCAG----- 541
Qy 143 AspLysGluLeuMetSerAspIleSerHisCysLeuGlyTyrSerLeuAspLysLeuGlu 162
Db 542 -----CGCCAGCTCAAGCCCTCATGCTGCTACGAGCTCACCGACGTCCAGC 586
Qy 163 GluSerLeuAspGluGluLeuArgGlnPheArgAlaSerLeuTrpAlaArgThrLysLys 182
Db 587 AACGTCATGACGATGAGACTG--GAGTTC-----ACGGCGGCC 622
Qy 183 ThrCysLeuThrArgGlyLeuGluGlyThrSerHisTyrAlaPheProGluGluGlnTyr 202
Db 623 CGCTGCTGAC----- 634
Qy 203 LeuCysValGlyGluSerCysProLysAspLeuGluSerLysValLysAlaLysLeu 222
Db 635 -----CCGCGCATGCGCGGAGGTGGCGCGGCGGACCCCAAGCTT 673
Qy 223 SerTyrGlnMetPheTrpArgLysArgLys-----AlaGluIle 235

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Db 674 TAGGCATGACCCCTGGGTGATCATCAAGCCCTCCTGAGTACCTTGTGAAGAATGC 733
 Qy 236 AanglyValCys-----GluysMetMetLysIleGlnIleGluPhe 249
 Db 734 ACTAACATCTGGCTTCATCTCATTCACCGCAGACCAAGCCAGCAATCAAGATGC 793
 Qy 250 AasnProAsnGluThrProLysSerLeuLeuH1sThrPheLeuTyrglyMetArgLys--- 268
 Db 794 TCGGCCGATGACACCCAGCAGCAGCATCTTCAGAGTTCTTTACCAAGATGGCCAAAG 853
 Qy 269 -----LeuAspValTyraSpThrAspProAlaAspGlnGlyTrpPheLeuGln 285
 Db 854 AATCTCTGATGATGATATCTCTGAAAGCCAGAACGAGGAG-----TTGTGCTGCAGC 907
 Qy 286 LeuAlaGlyArgThrThrPheValThrAsnProAspValLysLeuThrSerTyrgly 305
 Db 908 GTCGTGGCGCGGATGATGATCTGTGGGT---GAACGCCCATCAAAATTTCCAGTGG 964
 Qy 306 ValArgSerGluLeuGlnSerTyrglyTyrglyProGlyPheValValArgGlnSerLeu 325
 Db 965 GTGAGGAGTGCCTCAAGAT-----GGGAGAGATTCAC-----CTT 1003
 Qy 326 ValLeuLysAspTyrglyTyrglyProLysProLeuTyrglyProHisTyrglyValArgAlaHis 345
 Db 1004 GTGCTGAGC-----ACTCCTCAAGCCAGCCCTGAGCAG-----GTGAGGAAGAA 1051
 Qy 346 GluArgGlyLeuAlaLeuAspValLeuSerValSer-----IleAspSerThrProLys 363
 Db 1052 GAGTGGCCCGCTGGATGATGACACGAGGATGACCTGCTACCCAGCAGAGCTGACCAATC 1111
 Qy 364 GlnSerLysAsnSerAspMetValMetThrAspPheArgProThrAlaSerLeuLysGln 383
 Db 1112 CACGGCAAGGACCATGAAGATGTTCAC----- 1141
 Qy 384 ValSerLeuTrpAspLeuAspAlaLeuLeuMetIleArgProValAsnIleSerGlyPhe 403
 Db 1142 GTGCTCCTGTGGAGATGTGACCGCAAGTTCAGGGTCAAA-----ATCAGAGGCATT 1192
 Qy 404 AspPheProAla-----AspValAspMetTyrglyValArgIleGlnPheSerValTyrgly 420
 Db 1193 GATATCCCTGTCTCTGCCCCGAGCCGCTGACCTCAAGCTGTGTGTGAGGCAAAATCCAG 1252
 Qy 421 ValGlyThrLeuThrLeuAlaSerLysSerThrThr---LysValAsnIleGlnPheAla 439
 Db 1253 TATGGCAGCAAGTCTTTGCCAAGAGAAACAGCCCAACCTTCACAGAGAGAGTG 1312
 Qy 440 LysTrpAsnLysGluMetTyrglyThrPheAspLeuTyrglyMetLysAspMetProSerAla 459
 Db 1313 CTCTGGAAAGTGGGCTT---GAGTTCAGTATTAATCAAGAATTACCCAAAGGGGCT 1369
 Qy 460 ValLeuSerIleArgValLeuTyrglyLys-----Val 470
 Db 1370 CTGCTGAACCTTCAGATCTACTGCGGCAAGCTCCAGACCTGTCTGCAAGACCTTGTGA 1429
 Qy 471 LysLeuLysSerGlnGluPheGlu-----ValGlyTrpValAsnMetSer 485
 Db 1430 GAGATCCCAAGTCCCAAGTCCCAAGCAAGCAAGCTCACTTGTACTATGCTCAACTATG 1489
 Qy 486 LeuThrAspTrpArgAspGluLeuArgGlnGlyGlnPheLeuPheHisLeuTrpAlaPro 505
 Db 1490 CTGATAGACCAACGCTTCTCTGCGCCATGGGAGATGATGTCTCAACATGTGG----- 1543
 Qy 506 GluProThrAlaAsnArgSerArgIleGlyLys-----AanglyAlaArg 520
 Db 1544 -----CAGTTATCCGGGAAGGGGGAAGCAAGCAAGGAGCTTCATATGCCAAG 1591
 Qy 521 Ile-----GlyThrAsn-----AlaAlaValThrIleGluLysSer 532
 Db 1592 CTCACGTCGGGAACCAACCCGGAAGCAAGAGACTCAATGCTCAATCTTCATTTCTTGGAG 1651
 Qy 533 SerTyrglyValArgValArgMetProSerGlnGlyGlnTyrglyLeuValLysHis 552
 Db 1652 AATTACTGCAACCCATAGCTTGGCT-----AAGCAT 1684

Qy 553 ArgSerThrTrpThrGluThrLeuAsnIleMetGlyAspAspTyrglyLysCysLeuArg 572
 Db 1685 CGG-----CTAACCCCTGACCCAGAAAGGGACCGGCTTCGGGACGAATATGCC 1732
 Qy 573 AspProGlyTyrglyLysLeuGlnMetLeuValLysLysHisGlnSerGlyIleValLeu 592
 Db 1733 AATCAGCTTCGGAGCAACTGGAGCATCATAGCAGATCCGCTTAACCCACTACA 1792
 Qy 593 GluGluAspGluGlnArgHisIleValTrpMetTrpArg---ArgTyrglyIleGlnLysGlnGlu 611
 Db 1793 GCTGAAGCAAGAA-----CTGCTTGCAATTTCAATATGAAGGCTGAGAT 1843
 Qy 612 ProAspLeuLeuIleValLeuSerGluLeuAlaPheValTrpThrAspArgLysAsnPhe 631
 Db 1844 CCCAAAGCTATCTCAACTCTTTAGC---TCGGTGAATGGGAGCAGCAAGAAATTTGTG 1900
 Qy 632 SerGluLeuTyrglyValMetLeuGlnLys-----TrpLysProProSerValAlaAla 648
 Db 1901 GCCAAATCATCCATTTATTTAGCCAAAGGAGGTCTGGATCAGAGTCTTGTGATGTG 1960
 Qy 649 AlaLeuThr-----LeuLeuGlyLysArgCysThrAspArgValIleArgLysPheAla 666
 Db 1961 GGGTTAACCATGACACTCTGACTGCAACTTCTGATGTAAGAAAGCTGAGGCCATTGCA 2020
 Qy 667 ValGluLysLeuAsnGlnLeuSerProValThrPheHisLeuPheIleLeuProLeu 686
 Db 2021 GTCCAGAACTGGAGAGCTTGGAGATGATAGCTGTCCAT---TACTCTGCTCAGCTG 2077
 Qy 687 IleGlnAlaLeuLysTyrglyProArgAlaGlnSerGlnValGlyMetMetLeuLeuThr 706
 Db 2078 GTCCAGGCTGTGAATTTGAACCATGACATGACATGCGCTTACGACAGATTTCTGTGAAG 2137
 Qy 707 ArgAlaLeuCysAspTyrglyIleGlyHisArgLeuPheTrpLeuAlaGlnIle 726
 Db 2138 CGTGTTTAAGAAACAAAGAAATGTGTCACTTGTGTGTGTGTGTGTGAAGATGATG 2197
 Qy 727 AlaArgLeuArgAspCysAspLeuLysSerGlnGluTyrglyArgIleSerLeuLeuMet 746
 Db 2198 GCCCAGTCTAGG-----CACTATCAGCAAGAGTTTGCAGTATCTCTG 2239
 Qy 747 GluAlaTyrglyLeuArgGly---AsnGlnGlnHisIleLysIleIleThrArgGlnValAsp 765
 Db 2240 GAAAGCTTACCTGAGGGCGTGGCAGCAGCATGCTGCAAGCACTTCCACAGCAATGCCAA 2299
 Qy 766 MetValAspGluLeuThrArgIleSerThrLeuValLysGlyMetProLys----- 782
 Db 2300 GATATTTGACATGTTTCAAAAAGTCAACATTCATTAATGCTCTGCTGAAAAAGTAT 2359
 Qy 783 AspValAlaThrMetLysLeuArgAspGluLeuArgSerIleSerHisLysMetGlnAsn 802
 Db 2360 GAGCTCAGTTC-----CAAGTTATTTCCCACTTAAGCAAAAGCTTAAAAAC 2407
 Qy 803 MetAspSer-----ProLeuAspProValTyrglyLysLeu 813
 Db 2408 CTACAGAAATTTGAATCTCCCAAGCTTTAGTCTTATGCTTATGATCTGAGCTGAAGCC 2467
 Qy 814 GlyGluMetIleIleAspLysAlaIleValLeuGlySerAlaLysArgProLeuMetLeu 833
 Db 2468 GGGGCACTGGTGAATGAAAAAGTAAAGTGAAGGCTCCCAAGAAAGCCCTGAGGCT 2527
 Qy 833 HisTrpLysAsnLysAsnProLysSerAspHisIleLeuProPheCysAlaMetIlePhe 853
 Db 2528 GAGTTTAATGTGCCGATCTACGGCT---CTATCAATGAAGAAATTTGAATTTCTTT 2584
 Qy 854 LysAanglyAspAspLeuArgGlnAspMetLeuValLeuGlnValLeuGlnValMetAsp 873
 Db 2585 AAACAGGTGAGCATCTGGCCCAAGCATGCTTATTAAGATTTCAATCTCAATGAGAG 2644
 Qy 874 AsnIleTrpLysAlaAlaAsnIleAspCysLysLeuAsnProTyrglyAlaValLeuProMet 893
 Db 2645 TCCATTGGAGACCAAGATCTTGTGATCTGCTCTCCGCAATATGCTGATTCATCACT 2704

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Oy      894 G1YgUmetcIleg1Yle1eIG1ValVa1ProAnCySlytThr1lePheGlu1leGln 913
           |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      2705 GGTAACAATAATGAAGATATGACATCGTAAAGACGCCACACATGCCTAATAATTGAC 2764

Oy      . 914 ValGIYThrgIYPHeMeAsnThrAlaValArSerIlleaRProSerPHeMeAsnlys 933
           ---|||---|||---|||---|||---|||---|||---|||---|||---
Db      2765 CAAGAACA-----GTGGGCAACACGGGGT-----GCCTTAAAGATGAAGTCCTGAGTCAC 2815

Oy      934 Trp1leaRtgysGInCYSGdLYl1eGluAbRGLuYlsYlsYSerIvYlvAsRSeThr 953
           |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      2816 TGCGTCAAGAAAATAATGCCCTATTGAA--|||:::|||||:::|||||:::|||||::: 2845

Oy      954 LysAsnProliegIuYlvYsl1eaRAsnThrGlAlaMetYlvSYTY-PHeGluSer 973
           |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      2846 -----|||:::|||||:::|||||:::|||||:::|||||:::|||||::: 2860

Oy      974 ValAsPaRPhLeuTYrSeTySeCyValG1YrSeTyValAla1atrTYrl1eMetG1Yle 993
           |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      2861 GTTGAGAGATTTGGTTATTCCGTGGCCGGCTACTGTGTGGCAACCTTGTTCTCGGAATA 2920

Oy      994 LysAsPaRtgh1seSeAsPaSn1eMeTdeuthrGluAbRGLuYlsYTYValHs1leAsP 1013
           |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      2921 GGCAACAGACACATGACATATATATATATCTCAGAAACAGAAATCTATTCTATATTGAT 2980

Oy      1014 PHeG1YHs1leleugIYNHs1eG1LYeThrLysleugIYl1eGlnArGaSPArGlnPro 1033
           |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      2981 TTCCGACACATCTTGGGAATTACAAAGTTCTCGGGCATTAATAAAGAGAGGTGCCA 3040

Oy      1034 Phel1euthrGluNHs1ePHeMeThVAl1leaRserG1YusSeValAsPclYAsn 1053
           |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      3041 TTTGTGCTAACCCCAAGACTCTCTGTGTGTANG----GGGACTTCTGAAAGACACA 3094

Oy      1054 SerHs1eGluDeuGlnLYsPHeLySThrDeuCYSValGua1a1atYglVala1MeTTrpAsn 1073
           |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
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Oy      1074 AsnArGaSRleUPHeValSer1euPHeTh1eUwMetleugIYMecGluLeuProGluLeu 1093
           |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      3155 CACACAAACCCTACATCATCTCTCTTCCATGATGCTGAAGACAGAAAGATCCCCAGTTA 3214

Oy      1094 SerThryValaARleUAARleUAARHs1eleuYlvYThrLeuPHeCyAsnG1YgluSerLYs 1113
           |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      3215 ACCAGCAAAGAAGACATTGATATACATTGGGATGCCCTCACAGTC---GGCAAAAGTAG 3271

Oy      1114 GluGUla1aArGlyrPHePHeAlaG1YleTyGluGUla1aPHeAsnG1YSerTrpSer 1133
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Db      3272 GAGAGTCTTAAAAAGTAGTATTTCTGGATCAGATGAAGTTTCAGAGACAAAGATGGACC 3311

Oy      1134 ThrlyeThraNtTrlpHeNhs1alVal 1143
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Db      3332 GTGCAGTTTAACTGTTCTTACATCTGTT 3361

RESULT 12
US-08-972-G31-3
Sequence 3, Application US/08972631
Patent No. 5856133
GENERAL INFORMATION:
APPLICANT: Stephens, Len
APPLICANT: Hawkins, Phillip T.
TITLE OF INVENTION: G-BETA-GAMMA REGULATED
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 2730 Sand Hill Road
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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1	SOFTWAE: PatentIn Release #1.0, Version #1.30
2	CURRENT APPLICATION DATA:
3	APPLICATION NUMBER: US/08/972,631
4	FILING DATE:
5	CLASSIFICATION:
6	PRIOR APPLICATION DATA:
7	APPLICATION NUMBER: US 08/672,211
8	FILING DATE: 27-JUN-1996
9	ATTORNEY/AGENT INFORMATION:
10	NAME: Halliuh, Albert P.
11	REGISTRATION NUMBER: 25,277
12	REFERENCE/DOCKET NUMBER: 8549-0005-999
13	TELECOMMUNICATION INFORMATION:
14	TELEPHONE: (415)854-3660
15	TELEFAX: (415)854-3694
16	INFORMATION FOR SEQ ID NO: 3:
17	SEQUENCE CHARACTERISTICS:
18	LENGTH: 3808 base pairs
19	TYPE: nucleic acid
20	STRANDEDNESS: single
21	TOPOLOGY: unknown
22	MOLECULE TYPE: cDNA
23	US-08-972-631-3
24	Alignment Scores:
25	Pred. No.: 1.83e-113 Length: 3808
26	Percent: 1038.00 Matches: 316
27	Score Similarity: 46.96% Conservative: 224
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34	Qy 83 LeuHlAlaPwMetLysTrpGlyThrtYrSerValLysProGlnAspTYrValPheArg 102
35	Db 380 CTGGTCTTCCAGAGAGAGGGGAGAGTGTCACGAGTCTATGACAACTACCAAGTCCAGTGTG
36	Qy 103 GlnLeuAsnAspPheGlyGluHlleGluValHlePheAsnAspArgInProLeuSerLys 122
37	Db 440 ACCCTGAGCTGCGCTGCTGACTGAGGAGGTGTGCACCCGACCCCGGCGAGATCACGTG
38	Qy 123 LeuGlnLeuHlleGlyThrPheProMetLeuPheLeuTYrGlnProAspGlyHleAsnArg 142
39	Db 500 GTCCAGCGGACGCGCCCTCGAGAGACATTTGGCTTCCAG-----541
40	Qy 143 AspLysGlnLeuMetSerAspHlleSerHleCYsLeuGlyTYrSerLeuAspLysLeuGlu 162
41	Db 542 -----CGCCAGCTCAACCCCTTCATCGGCTTACGACGTACCGACGACGTGACG 586
42	Qy 163 GluSerLeuAspGlnGlnLeuArgGlnPheArgAlaSerLeuTrpAlaArgThrLysLys 182
43	Db 587 AACGTGCATGACGATGACTG---GAGTTC-----ACCGGGCGC 622
44	Qy 183 ThrCYsLeuThrArgGlyLeuGlnGlnLysSerHleTYrAlaPheProGlnGlnIntyr 202
45	Db 623 CGCTGTGTACCC-----634
46	Qy 203 LeuCYsValGlyGluSerCYsProLysAspLeuGlnSerLysValLysAlaAlaLysLeu 222
47	Db 635 -----CCGCGCATGGCCGAGGTGGCGGCGCGGACCCCACTT 673
48	Qy 223 SerTYrGlnMetPheTrpArgLysArgLys-----AlaGlnHle 235
49	Db 674 TACGCATGACCCCTGGGTGATCATCCAAAGCCCTCCCTGATGATCCTTGAGAGAAATC 733
50	Qy 236 AsnGlyValCYs-----GlnLysMetMetLysHlleGlnHleGluPhe 249
51	Db 734 ACTTAAACATGTGGTCTTCATGCTCATGACCGGACGACACCAAGCCAGACATCAAGTGC 793

QY 269 -----LeuaspValTyrAspThrAspProAlaAspGluGlyTyrPheLeuGln 285
 Db 884 AAATCTGATGATATCCCTGAGAACCAAGAACGAGAC-----TTTGTCTGGCC 907
 QY 286 LeuAlaGlyArgThrPheValThrAspProValTyrLeuThrSerTyrAspGly 305
 Db 908 GTCTCGCGCGCGGAGATGACTGCTGGTGGT---GAGAGCGCCATCAAAATTTCCAGTGG 964
 QY 306 ValArgSerGluLeuGluSerTyrArgCysProGlyPheValValArgArgGlnSerLeu 325
 Db 965 GTGAGCGAGTGCCTCAGAAAT-----GGGAGAGAGATTAC-----CTT 1003
 QY 326 ValLeuLysAspTyrCysArgProLysProLeuTyrGluProHisTyrValArgAlaHis 345
 Db 1004 GTTCTGGAC-----ACTCTCCAGACCCAGCCCTGGACGAG-----GTGAGAGAGAA 1051
 QY 346 GluArgLysLeuAlaLeuAspValLeuSerValSer-----LAspSerThrProLys 363
 Db 1052 GAGTGGCGCGCTGTGGATGACTGCAAGGAGTCACTGGCTTACAGAGAGCTGACATC 1111
 QY 364 GlnSerLysAsnSerAspMetValMetThrAspPheArgProThrAlaSerLeuLysGln 383
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 QY 384 ValSerLeuTyrAspLeuAspAlaAsnLeuMetIleArgProValAsnIleSerGlyPhe 403
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 Db 1193 GATATCCCTGTCTGCGCCCGGACCGCTGACCTCAGCGTGTGTGGAGCAAAATCCAG 1252
 QY 421 ValGlyThrLeuThrLeuAlaSerLysSerThrThr--LysValAsnAlaGlnPheAla 439
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 QY 460 ValLeuSerIleArgValLeuTyrGlyLys-----Val 470
 Db 1370 CTGCTGAACCTCCAGATCTACTGCGGCAAGCTCCAGACGTCTGGCAAGACCTCTGCA 1429
 QY 471 LysLeuLysSerGluLysGluPheGlu-----ValGlyTyrValAsnMetSer 485
 Db 1430 GAGATGCCAGTCCCGAGTCCAAAGGCAAGCTCACTTCTGATCTATCTCAACCTATTG 1489
 QY 486 LeuThrAspTyrArgAspGluLeuArgGlnGlyGlnPheLeuPheHisLeuTyrAlaPro 505
 Db 1490 CTGATAGACACCGCTTCTCTGCGCCATGGCGAGTATGTCTCCACATGTGG----- 1543
 QY 506 GlnProThrAlaAsnArgSerArgIleGlyGlu-----AsnGlyAlaArg 520
 Db 1544 -----CAGTTATCCGGAGAGGGGAGAACCAAGGAGCTTCAATGCCGACAG 1591
 QY 521 Ile-----GlyThrSer-----AlaAlaValThrIleGluIleSer 532
 Db 1592 CTCACGCTCGGAAACCAACCCGCAAGAGACTCAATGTCTCCATCTCTTCTGGAC 1651
 QY 533 SerTyrGlyArgValArgMetProSerGlnGlyGlnTyrThrTyrLeuValLysHis 552
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 QY 553 ArgSerThrTyrThrGluThrLeuAsnIleMetGlyAspAspTyrGlnSerCysIleArg 572
 Db 1685 CCG-----CCTACCCCTGACCAAGAGGAGCGGAGTGGCGAGAAATGCC 1732
 QY 573 AspProGlyTyrTyrLysLeuGlnMetLeuValLysHisGlnSerGlyIleValLeu 592
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 QY 593 GlnGluAspGlnGlnArgHisValTyrMetTyrArg--ArgTyrIleGlnLysGlnGlu 611

Db 1793 GCTGAAGCAAGAA-----CTGCTCGCATTTCAATATGAAGCTGAAGAT 1843
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 Db 1901 GCCAAACATTCACATTAATTAAGCCAAAGGAGAGTCTGGAGTCAAGATCTTGGATGTG 1960
 QY 649 AlaLeuThr-----LeuLeuGlyLysArgCysThrAspArgValIleArgLysPheAla 666
 Db 1961 GGGTTAACCATGACAGCTCTCTGACTGCAACCTTCGGATGAAGACGTAAGACCATTCGA 2020
 QY 667 ValGluLysLeuAsnGlnGluLeuSerProValThrPheHisLeuPheIleLeuProLeu 686
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 Db 2078 GTCCAGGCTGTGAATTTGAACCATACCATGACAGTGCCTTACGACATTTCTGCTGAAG 2137
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 US-08-972-630-3
 ; Sequence 3, Application US/08972630
 ; Patent No. 5869271
 ; GENERAL INFORMATION:
 ; APPLICANT: Stephens, Len
 ; APPLICANT: Hawkins, Phillip T.
 ; TITLE OF INVENTION: G-BETA-GAMMA REGULATED
 ; TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 2730 Sand Hill Road
 ; CITY: Menlo Park
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94025
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/972,630
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/672,211
 ; FILING DATE: 27-JUN-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Halluin, Albert P.

; REGISTRATION NUMBER: 25,277
 ; REFERENCE/DOCKET NUMBER: 8549-0005-999
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415)854-3660
 ; TELEFAX: (415)854-3694
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3808 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: cDNA
 ; US-08-972-630-3
 Alignment Scores:
 Pred. No.: 1,836-113 Length: 3808
 Score: 1038.00 Matches: 316
 Percent Similarity: 46.96% Conservative: 224
 Best Local Similarity: 27.48% Mismatches: 400
 Query Match: 17.17% Indels: 210
 DB: 2 Gaps: 46
 US-08-908-453-1 (1-1146) x US-08-972-630-3 (1-3808)
 Qy 68 SerLeuGlnIleLysLeuSer---AspPheLysHisGlnLeu-----PheGlu 82
 Db 320 GCGCTGGAGAGAGAGGTTCTTGGGACTTCTTACCAACGGCTTCGCGCCGACCACTTCTC 379
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 Db 635 -----CCGGCATGCGCGAGGTGGCGGCGCGGACCCCAAGCTT 673
 Qy 223 SerTyrGlnMetPheTrpArgLysArgLys-----AlaGlnIle 235
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      593 GlnGluAspGluGlnArgHisValaTyrMetTyrArg--ArgTyrLLeGlnLysGlnGlu 611
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      667 VALGluLysLeuAsnGluGlnLeuSerProValThrPheHisLeuPheLLeuProLeu 686
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 6, 2003, 05:04:05 ; Search time 852 Seconds

(without alignments)
1882.476 Million cell updates/sec

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Database : Published Applications_NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	6046	100.0	3504	US-09-205-658-47	Sequence 47, Appl
2	6046	100.0	3504	US-09-844-353A-47	Sequence 47, Appl
3	1033	17.1	5220	US-10-027-591-1	Sequence 1, Appl
4	1031	17.1	3387	US-10-162-160-2	Sequence 2, Appl

5	668	11.0	5990	US-09-917-800A-477	Sequence 477, App
6	624	10.3	5061	US-10-092-219-1	Sequence 1, Appl
7	551.5	9.1	3252	US-09-921-332-1	Sequence 1, Appl
8	551.5	9.1	3252	US-09-921-330-1	Sequence 1, Appl
9	551.5	9.1	3252	US-09-921-329-1	Sequence 1, Appl
10	399	6.6	2418	US-09-771-161A-10	Sequence 10, Appl
11	325	5.4	5703	US-09-801-368-389	Sequence 389, App
12	309	5.1	2620	US-09-925-102-205	Sequence 205, App
13	278	4.6	7864	US-09-834-975-805	Sequence 805, App
14	257.5	4.3	2451	US-09-976-165-29	Sequence 32, Appl
15	257.5	4.3	2487	US-09-976-165-32	Sequence 32, Appl
16	257.5	4.3	3624	US-09-976-165-33	Sequence 33, Appl
17	257.5	4.3	3602	US-09-976-165-30	Sequence 30, Appl
18	228	3.8	339	US-09-796-692-7359	Sequence 7359, App
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20	218.5	3.6	9385	US-10-175-225-1	Sequence 1, Appl
21	215.5	3.6	9171	US-09-810-993-1	Sequence 1, Appl
22	215.5	3.6	9196	US-08-984-090-1	Sequence 1, Appl
23	215	3.6	326	US-09-796-692-7451	Sequence 7451, App
24	215	3.6	326	US-10-040-862-7451	Sequence 7451, App
25	191.5	3.2	3423	US-09-950-634-2	Sequence 2, Appl
26	191.5	3.2	7653	US-09-950-634-1	Sequence 1, Appl
27	191.5	3.2	8741	US-10-198-846-11285	Sequence 11285, App
28	186.5	3.1	441	US-09-867-701-5505	Sequence 5505, App
29	179.5	3.0	8838	US-09-957-837A-1	Sequence 1, Appl
30	178.5	3.0	4074	US-09-764-877-3796	Sequence 3796, App
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34	154.5	2.6	4651	US-09-957-837A-3	Sequence 3, Appl
35	154.5	2.6	4651	US-09-957-837A-5	Sequence 5, Appl
36	141	2.3	2970	US-10-270-333-133	Sequence 133, App
37	139	2.3	3640	US-09-297-758-144	Sequence 144, App
38	137	2.3	466	US-09-918-995-35578	Sequence 35578, App
39	136	2.2	3859	US-10-097-340-3	Sequence 3, Appl
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41	136	2.2	3859	US-09-864-864-300	Sequence 300, App
42	130.5	2.2	4424	US-10-245-115-1	Sequence 1, Appl
43	129.5	2.1	3720	US-10-076-622-576	Sequence 576, App
44	129.5	2.1	3720	US-10-007-805-576	Sequence 576, App
45	128	2.1	436	US-09-918-995-857	Sequence 857, App

ALIGNMENTS

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RESULT 1
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; Patent No. US20010029617A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Osg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; FILE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 3504
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-09-205-658-47
Alignment Scores: 0
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Length: 3504

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Score: 6046.00 Matches: 1146
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 DB 1624 ATAGGACACCAACGCGCGGTTCACATTTGAAATCTCAAGTGTGTGTGTGTGTGTGTGTGT 1683
 QY 541 ProSerGlnGlyGlnTrpThrTrpLeuValLysHisArgSerThrTrpGlnThrLeu 560
 DB 1684 CCGAGTCAAGGCAATACATATCTGTCAACGCCAAGTACTTGAACGGAACCTTGG 1743
 QY 561 AsnIleMetGlyAspAspTrpGlnSerCysIleArgAspProGlyTrpLysLysLeuGln 580
 DB 1744 AATATTATGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1803
 QY 581 MetLeuValLysLysHisGlnSerGlyLysValLeuGlnGlnAspGlnGlnArgHisVal 600
 DB 1804 ATGCTTGTCAAGACATGAATCTGGAATTTGATTAAGGAAGAAAGAAACAGTATATGTC 1863
 QY 601 TrpMetTrpArgArgTrpIleGlnLysGlnGlnProAspLeuLeuIleValLeuSerGln 620
 DB 1864 TGGATGTGAGAGATACATTCAAAGCAAGAGCTGATTTGTCTATTTGTCTCTCCGAA 1923
 QY 621 LeuAlaPheValTrpThrAspArgGlnAsnPheSerGlnLeuTrpValMetLeuGlnLys 640
 DB 1924 CTCGCAATTTGTGTGACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1983
 QY 641 TrpLysProProSerValAlaAlaAlaLeuThrLeuLeuGlnGlyLysCysThrAspArg 660
 DB 1984 TGGAAACGCGCAGGTGTGGACGCGCGGTGTGCTTGTGGAAAAAGCTTGGACGATGCT 2043
 QY 661 ValIleArgLysPheAlaValGlnLysLeuAsnGlnGlnLysSerProValThrPheHis 680
 DB 2044 GTGATTCGAAGTTTTCAGTGGAGAGTTGAATGAGAGCTGAGCCGCTGACATTTCCAT 2103
 QY 681 LeuPheIleLeuProLeuIleGlnAlaLeuLysTrpGlnProArgAlaGlnSerGlnVal 700

Db 2104 CTTTCATATGCTCTCATACAGCGCTTGAAAGTACGACCGCTGCTCAATCGAGATT 2163
 Qy GlyMetMetLeuLeuThrArgAlaLeuCysAspTyrArgIleGlyHisArgLeuPheTyr 720
 Db 2164 GGATGATGCTCTTACTAGAGCTCTGCGCATATCGAATGGACATCGAGCTTTTCGG 2223
 Qy LeuLeuArgAlaGluIleAlaArgLeuArgAspCysAspLeuLysSerGluGlyTyrArg 740
 Db 2224 CTGCTCCGTGACAGATTGCTGTTGAGAGATTGTGATCTGAAAAGTGAAGAAATATGCG 2283
 Qy ArgIleSerLeuLeuMetGluAlaTyrLeuArgGlyAsnGluGlyHisIleLysIleIle 760
 Db 2284 CGTATCTCACTCTGATGGAAGCTTACCTCCGTGAAATGAAAGACACATCAAGTATCATC 2343
 Qy ThrArgGlnValAspMetValAspGluLeuThrArgIleSerThrLeuValIleGlyMet 780
 Db 2344 ACCGACAAAGTTGACATGATGATGAGCTCACACAAATCGACATCTTGTCAAAGGAATG 2403
 Qy ProLysAspValAlaThrMetLysLeuArgAspGluLeuArgSerIleSerHisLysMet 800
 Db 2404 CCAAAAGATGTTGCTACGATGAACTGGGTGACGAGCTTCGATTCGATTAGTATTAATG 2463
 Qy GluLeuMetAspSerProLeuAspProValTyrLysLeuGlyGluMetIleLeuAspLys 820
 Db 2464 GAAATATGATTCCTCCACTGATCTGTGTACAAACTGGGTGAATGATATATACACAA 2523
 Qy AlaIleValIleGluSerAlaLysArgProLeuMetLeuHisIleTyrLysAsnLysAsnPro 840
 Db 2524 GCCATGCTCTTAGAAGAGTCAAAAGCTGTTAATGCTTCACTGGAAGAAACAAATATCA 2583
 Qy LysSerAspLeuHisIleLeuProPheCysAlaMetIlePheLysAsnGlyAspAspLeuArg 860
 Db 2584 AAGAGTGACCTGCACTTCCTGTCGCAATGATCTTCAAGAAATGGAGAGCATTTTGGC 2643
 Qy GluAspMetLeuValLeuGlnValLeuGluValMetAspAsnIleTyrLysAlaAlaAsn 880
 Db 2644 CAGGACATGCTGTTCTTCAAGTTCTCGAAGTTATGATGATTAATCGAAGAGCTGCAAC 2703
 Qy IleAspCysValLeuAsnProTyrAlaValLeuProMetGlyGluMetIleGlyIleIle 900
 Db 2704 ATTGATCTGTTTAAACCCGATCCAGTCTTCCAAATGGGGAAGAAATATGGAATATAT 2763
 Qy GluValValProAsnCysLysThrIlePheGluIleGlnValGlyThrGlyPheMetAsn 920
 Db 2764 GAAGTGGCGCTAATGTTAAACATATTCGAGATTCGAAGTTGGAACGAGATTCATGAT 2823
 Qy ThrAlaValArgSerIleAspProSerPheMetAsnLysTyrIleArgLysGlnCysGly 940
 Db 2824 ACAGCAGTTCGAGATGATGATCTTCTGTTATGAAATTAAGTGGATTCGAAAACATGCGGA 2883
 Qy IleGluAspGluValLysSerLysValAspSerThrLysAsnProIleGluLysLys 960
 Db 2884 ATTGAAGATGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 2943
 Qy IleAspAsnThrGlnAlaMetLysLysTyrPheGluSerValAspArgPheLeuTyrSer 980
 Db 2944 ATTGATATATCTCAAGCATGAAAGAAATATTTTGAAGTGTGATCGATTCCTATACG 3003
 Qy CysValGlyTyrSerValAlaThrTyrIleMetGlyIleLysAspArgHisSerAspAsn 1000
 Db 3004 TGTGTTGATATATTCAGTTCACGCTACATTAATGGAAATCAAGATCGTACACAGTATAT 3063
 Qy LeuMetLeuThrGlnAspGlyLysTyrValHisIleAspPheGlyHisIleLeuGlyHis 1020
 Db 3064 CTGATGCTCACTGAAGATGAAGAAATATGTCACATGATATTCGGTCACTTTTGGGACAC 3123
 Qy GlyLysThrLysLeuGlyIleGlnArgAspArgGlnProPheIleLeuThrGlnHisPhe 1040
 Db 3124 GGAAGAACCAAACTGGGATCGAGGAGATGTCACACGTTATATCTAAACGAAACACTT 3183
 Qy MetThrValIleArgSerGlyLysSerValAspGlyAsnSerHisGluLeuGlnLysPhe 1060
 Db 3184 ATGACAGATGATTCATCGGATTAATCTGTGATGAAATTCGATGAGCTACAAAATTC 3243

Qy 1061 LysThrLeuCysValGluAlaTyrGluValMetTyrAsnAsnArgAspLeuPheValSer 1080
 Db 3244 AAAAGCTTATCCGTCGAAGCTTACGAAGTATGTGGAATATCGAATTTGTCTTCC 3303
 Qy 1081 LeuPheThrLeuMetLeuGlyMetGluLeuProGluLeuSerThrLysAlaAspLeuAsp 1100
 Db 3304 TTGTTACCTTGAATGCTCGGAATGAGATGGCTGAGGCTGTGACGAAAGCGGATTTGGAT 3363
 Qy 1101 HisLeuLysLysThrLeuPheCysAsnGlyGluLysTyrGluGluAlaArgLysPhePhe 1120
 Db 3364 CATTGAAGAAACCTCTTTCGAATGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGTTC 3423
 Qy 1121 AlaGlyIleTyrGluGluAlaPheAsnGlySerTyrPheSerThrLysAsnTyrLeuPhe 1140
 Db 3424 GCTGGAATCTGGAAGAAAGCTTCAATGATCATGCTACCAAAACGAATTTGCTTTC 3483
 Qy 1141 HisAlaValLysHisTyr 1146
 Db 3484 CACGACATCAACACTAC 3501

RESULT 2

US-09-844-353A-47
 ; Sequence 47, Application US/09844353A
 ; Patent No. US20020037585A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruvkun, Gary
 ; APPLICANT: Kimura, Koutarou
 ; APPLICANT: Paterson, Garth
 ; APPLICANT: Ogg, Scott
 ; APPLICANT: Paradise, Suzanne
 ; APPLICANT: Tissenbaum, Heidi
 ; APPLICANT: Morris, Jason
 ; APPLICANT: Kowek, Allison
 ; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
 ; FILE REFERENCE: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
 ; CURRENT APPLICATION NUMBER: US/09/844,353A
 ; PRIOR FILING DATE: 2001-04-27
 ; PRIOR APPLICATION NUMBER: US 08/857,076
 ; NUMBER OF SEQ ID NOS: 114
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 47
 ; LENGTH: 3504
 ; TYPE: DNA
 ; ORGANISM: Caenorhabditis elegans
 US-09-844-353A-47

Alignment Scores:

Pred. No.: 0 Length: 3504
 Score: 6046.00 Matches: 1146
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-08-908-453-1 (1-1146) x US-09-844-353A-47 (1-3504)

Qy 1 MethiValAsnIleLeuHisArgGlnLeuGlnThrMetValGluGlnTyrGlnMetArg 20
 Db 64 ATGATGTTAATCATTTTACATCCCAACTGCAAAAGATGTCGAGCATGCAATGCGA 123
 Qy 21 GluArgProSerLeuGluThrGlnAsnGlyLysGlySerLeuLeuLeuGluArgGly 40
 Db 124 GAAAGCCCATCGCTGGAAGACCGAAGATGGCAAGATCGCTCCGGAAGAAATGAAGCT 183
 Qy 41 ValAlaAspIleIleThrMetCysProPheGlyGluValIleSerValAlaPheProTyr 60
 Db 184 GTCCGAGTATCATCATATGTCTCATTCGGAAGATTTATTAATGTATTTCCGTGG 243
 Qy 61 PheLeuAlaAsnValArgThrSerLeuGluIleLysLeuSerAspPheLysGlnLeu 80

Db 244 TTTCTGCAATGTGCGAATCATGCTAGAAATCAAGTATTCAGATTTTCAAAACATGACTT 303
 Qy 81 PheGluLeuIleAlaProMetLysTrpGlyThrTyrSerValLysProGlnAspTyrVal 100
 Db 304 TTCGAATGATTGCTCCGATGAGATGGGGAACATATTCGTTAAACCCACAGATTATGTG 363
 Qy 101 PheArgGlnLeuAsnAspPheGlyGluIleGluValIlePheAsnAspAspGlnProLeu 120
 Db 364 TTCAGACAGTTAAATTAATTCGCGCAAAATGGAATTAATTAAGACATCAACCCCTG 423
 Qy 121 SerLysLeuGluLeuHisGlyThrPheProMetLeuPheLeuTyrGlnProAspGlyIle 140
 Db 424 TCGAAATTAAGACTCCACGGCACTTTCCCAATGCTTTTCTCTACCAACTGATGGAATA 483
 Qy 141 AsnArgAspLysGluLeuMetSerAspLysSerHisGlyLeuGlyTyrSerLeuAspLys 160
 Db 484 AACAGGATTAAGAAATTAATGAGTGAATTAAGTCAATTCCTAGGATACCTGAGATAAA 543
 Qy 161 LeuGluGlnSerLeuAspGlnGluLeuArgGlnPheArgAlaSerLeuTrpAlaArgThr 180
 Db 544 CTGGAAGAGAGCTCGATGAGAACTCCGTCAAATTCGTCTCTCTGGGCTGTAG 603
 Qy 181 LysLysThrCysLeuThrArgLysLeuGluGlyThrSerHisTyrAlaPheProGluGln 200
 Db 604 AAGAAACGCTGCTTGACAGTGAAGTGAAGGATCAAGTCACTAGCCGTTCCCGAAGA 663
 Qy 201 GlnTyrLeuCysValGlyGlnSerCysProLysAspLeuGlnSerLysValIleAla 220
 Db 664 CAGTCTTGTTGTGTGGTGAATCGTGCCGAAAGATTGGAAATCAAAAGTCAAGGCTGCC 723
 Qy 221 LysLeuSerTyrGluMetPheTrpArgLysArgLysAlaGluIleAsnGlyValCysGlu 240
 Db 724 AAGCTGAGTTACAGATGTTTGGAGAAACGTAAGCCGAATCAATGAGATTTGCGAG 783
 Qy 241 LysMetMetLysIleGlnIleGluPheAsnProAsnGlnThrProLysSerLeuLeuHis 260
 Db 784 AAAATGATGAAAGTTCAATTAATTCATCCGAAGAACTCCGAATCTCGCTTCAAC 843
 Qy 261 ThrPheLeuTyrGluMetCysLysLeuAspValTyrAspThrAspAspProAlaAspGlu 280
 Db 844 AGCTTCTCTACGAAATGCGAAATTTGATGATACGATACCGATATCTCTCAGATGAA 903
 Qy 281 GlyTrpPheLeuGlnLeuAlaGlyArgThrThrPheValThrAsnProAspValLysLeu 300
 Db 904 GGAATGTTCTTCAATGCTGAGACGTACCACTTTGTTCAAAATCAAGTCCAAACTT 963
 Qy 301 ThrSerTyrAspGlyValArgSerGluLeuGlnSerTyrArgCysProGlyPheValVal 320
 Db 964 AGCTTATGATGATGCTGCTCGGAACTGGAAGCTATCGATGCCCTGGAATTCGTTGT 1023
 Qy 321 ArgArgGlnSerLeuValLeuLysAspTyrCysArgProLysProLeuTyrGluProHis 340
 Db 1024 CCGCGCAATCACTACTCTCTCAAGACTATTTGTCGCGCAAAACCACTTACGAACCAACT 1083
 Qy 341 TyrValArgAlaHisGluArgLysLeuAlaLeuAspValLeuSerValSerIleAspSer 360
 Db 1084 TATGTGAGACACACGAACGAACCTGCTAGACGTGCTCAGCTGCTCTATAGATAC 1143
 Qy 361 ThrProLysGlnSerLysAsnSerAspMetValMetThrAspPheArgProThrAlaSer 380
 Db 1144 ACACCAAAACAGAGCAAGAACAGTGCATGTTATGATGATTTTGTCTCGACAGCTTCA 1203
 Qy 381 LeuLysGlnValSerLeuThrAspLeuAspAlaAsnLeuMetLysArgProValAlaIle 400
 Db 1204 CTCAAACAAAGTTCACTTGGGACTTTCGAGCGCAATCTTAATGATAGGCTGTGATATT 1263
 Qy 401 SerGlyPheAspPheProAlaAspValAspMetTyrValArgIleGluPheSerValTyr 420
 Db 1264 TCTGATTTGATTTCCCGGCGCACTGATATGTACGTTGCAATTCAGATGATAT 1323
 Qy 421 ValGlyThrLeuThrLeuAlaSerLysSerThrThrLysValAsnAlaGlnPheAlaLys 440
 Db 1324 GTGGGAGACCTGACGCTGGCATCAAAATCTACAAACAAAGTGAATGCTCAATTTGCAAAA 1383

Qy 441 TrpAsnLysGluMetTyrThrPheAspLeuTyrMetLysAspMetProProSerAlaVal 460
 Db 1384 TGGAAATGAAGAAATGACTTTTGAATCTATACATGAAGGATATGACCAATCTGCACATA 1443
 Qy 461 LeuSerIleArgValLeuTyrGlyLysValLysLeuLysSerGluGluPheGluValGly 480
 Db 1444 CTCAGCATTCGTGTTTGTACGAAAGTGAATTTAAAGATGAAGATTCGAATTCGT 1503
 Qy 481 TrpValAsnMetSerLeuThrAspTrpArgAspGluLeuArgGlnGlyGlnPheLeuPhe 500
 Db 1504 TGGGTAATATATGCTCCATACCGATGAGATCAATCACTACACAGACAAATTTTATTC 1563
 Qy 501 HisLeuTrpAlaProGluProThrAlaAsnArgSerArgIleGlyLysAsnGlyValArg 520
 Db 1564 CATCTGTGGGCTCTGAAACCACTGCAATCTGATGATGATGAGAAATGAGACAGG 1623
 Qy 521 IleGlyThrAsnAlaAlaValThrIleGluLysSerSerTyrGlyArgValArgMet 540
 Db 1624 ATAGGCACCAACGACGCGTTACAAATTAATCTCAAGTATGATGATGATGATGATG 1683
 Qy 541 ProSerGlnGlyGlnTyrThrTyrLeuValLysHisArgSerThrTrpThrGluThrLeu 560
 Db 1684 CCGAGTCAAGACAAATACATATCTGTCACAGACCCGAACTGTCGACGGAACCTTGG 1743
 Qy 561 AsnIleMetGlyAspAspTyrGlnSerCysIleArgAspProGlyTyrLysLysLeuGln 580
 Db 1744 AATATTAATGAGGATGATTAATGATGATGATGATGATGATGATGATGATGATGATG 1803
 Qy 581 MetLeuValLysLysHisGlnSerGlyIleValLeuGluGlnAspGluGlnArgHisVal 600
 Db 1804 ATGCTTGTCAGAAAGCATGAAATTCGAAATTTATTAAGGAATGAACCAACGTCATGTC 1863
 Qy 601 TrpMetTrpArgGlyTyrIleGlnLysGlnGluProAspLeuIleValLeuSerGlu 620
 Db 1864 TGGAGTGCAGAGATACATCAAAAGCAGAGCTGATTTGCTCATGTCCTCTCCAA 1923
 Qy 621 LeuAlaPheValTrpThrAspArgGluAsnPheSerGluLeuTyrValMetLeuGluLys 640
 Db 1924 CTCGCATTTGTGTGACTGATCTGAGAACTTTCCAGCTCTATGTGATGCTTGAAAA 1983
 Qy 641 TrpLysProProSerValAlaAlaLeuThrLeuLeuGluGlyLysArgCysThrAspArg 660
 Db 1984 TGGAAACCGCGAGTGTGCGACCGCGCTGATCTTGTGAAAAACGTTGACCGATCGT 2043
 Qy 661 ValIleArgLysPheAlaValGluLysLeuAsnGluGlnLeuSerProValThrPheHis 680
 Db 2044 GTGATTCGAAAGTTTGCAGTGAAGATTTGAATGAGCAGTGAAGCCGCTCACAATTCAT 2103
 Qy 681 LeuPheIleLeuProLeuIleGlnAlaLeuLysTyrGluProArgAlaGlnSerGluVal 700
 Db 2104 CTTTTCATATTCCTCTCTATACAGGCTTGGAATGACGCGCTGCTCAATTCGAAATT 2163
 Qy 701 GlyMetMetLeuLeuThrArgAlaLeuCysAspTyrArgIleGlyHisArgLeuPheTrp 720
 Db 2164 GGAATGAGCTCTTACATAGAGCTCTGCGCAATTAATGAATGACATCGACTTTTCGG 2223
 Qy 721 LeuLeuArgAlaGluIleAlaArgLeuArgAspCysAspLeuLysSerGluGluTyrArg 740
 Db 2224 CTGCTCCGTGACAGAAATGCTGCTTGAAGATTTGATCTGGAAGAAAGGAATATGC 2283
 Qy 741 ArgIleSerLeuLeuMetGluAlaTyrLeuArgLysAsnGluGluHisIleLysIleIle 760
 Db 2284 GGTATCTCACTCTGATGAGAGCTTACCTCCGTGAAATGAAGACACATCAAGATCTC 2343
 Qy 761 ThrArgGlnValAspMetValAspGluLeuThrArgIleSerThrLeuValLysGlyMet 780
 Db 2344 ACCGCAAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2403
 Qy 781 ProLysAspValAlaThrMetLysLeuArgAspGluLeuArgSerIleSerHisLysMet 800
 Db 2404 CCAAAAGATGTTGTACATGAAGAACTGGTGACGAGCTTCATGATTAATGATTAATG 2463

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QY 801 GluAenMetAspSerProLeuAspProValTyrIleuLeuGluMetIleIleAspLys 820
Db 2464 GAAATATATGATTCCTCCACTGATCTCTGTATCAAACTGGGTAATATATCCGCAAA 2523
QY 821 AlaIleValleuGlySerAlaLysArgProLeuMetLeuHisTyrLysAsnLysAsnPro 840
Db 2524 GCCATCGCTCAGAGAGGCAAAACGCTCGTTAAAGCTTCACATGGAAGCAAAATCCA 2583
QY 841 LysSerAspLeuHisIleuProPheCysAlaMetIlePheLysAsnGlyAspAspLeuArg 860
Db 2584 AAGATGACCTGACCTTCCTGCTGTCGCAATGATCTTCAGAAAGAGACATCTTCGC 2643
QY 861 GluAspMetLeuValleuGluValleuGluValleuMetAspAsnIleTyrLysAlaAsn 880
Db 2644 CAGGACATGCTTCTTCCTCAAGTTCGAAAGTTAAGATTAATCATCGAAGGCTCCAAAC 2703
QY 881 IleAspCysCysLeuAsnProTyrAlaValleuProMetGlyGluMetIleGlyIleIle 900
Db 2704 ATTGATTCGTGTTTAAACCCGTAACGAGTTCTTCAATGGGAGAAATGATTCGAATTAT 2763
QY 901 GluValValProAsnCysLysThrIlePheGluIleGluValGlyThrGlyPheMetAsn 920
Db 2764 GAAATTCGCTTAATGTAAACAAATATCGAGATTCAGTTGGAACAGGATTCATGAT 2823
QY 921 ThrAlaValArgSerIleAspProSerPheMetAsnLysTyrIleArgLysGlnCysGly 940
Db 2824 ACAGCAGTTCGGAGATTCATCTCTGTTATGAATTAAGTGAATTCGGAACAAATCCGGA 2883
QY 941 IleGluAspGluLysLysLysSerLysLysAspSerThrLysAsnProIleGluLysLys 960
Db 2884 ATTGAAGTGAAGAAAGCAAAAGCAAAAGCACTACCAAAATCCCTCCAAAGAGAG 2943
QY 961 IleAspAsnThrGluAlaMetLysLysTyrPheGluSerValAspArgPheLeuTyrSer 980
Db 2944 ATTGATTAATCTCAACCCAGCAAGCAAGATTTTGAAGTGTGATGATTCCTAATACCG 3003
QY 981 CysValGlyTyrSerValAlaThrTyrIleMetGlyIleLysAspArgHisSerAspAsn 1000
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QY 1001 LeuMetLeuThrGluAspGlyLysTyrValHisIleAspPheGlyHisIleLeuGlyHis 1020
Db 3064 CTGATGCTCAGCAAGATGAGAAATATGTCACATTCGTCACATTTTGGGACAC 3123
QY 1021 GlyLysThrLysLeuGlyIleGlnArgAspArgGlnProPheIleLeuThrGluHisPhe 1040
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QY 1041 MetThrValIleArgSerGlyLysSerValAspGlyAsnSerHisGluLeuGlnLysPhe 1060
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Db 3244 AAAAGTTATGCGTGAAGCTTACGAAAGTAAATGGAATTAATCGAATTTGTTCC 3303
QY 1081 LeuPheThrLeuMetLeuGlyMetGluLeuProGluLeuSerThrLysAlaAspLeuAsp 1100
Db 3304 TTGTTCACCTTGATCTCGAATGAGATTCCTGAGCTGTTCAGCAAAAGCGGATTTGAT 3363
QY 1101 HisLeuLysLysThrLeuPheCysAsnGlyGluSerLysGluGluAlaArgLysPhePhe 1120
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QY 1121 AlaGlyIleTyrGluGluAlaPheAsnGlySerTyrPheSerThrLysThrAsnTyrLeuPhe 1140
Db 3424 GCTGCAATCTACGAAGAGCTTCATGATGATGATGATGATGATGATGATGATGATGAT 3483
QY 1141 HisAlaValLysHisTyr 1146
Db 3484 CACGAGTCACCACTAC 3501

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US-10-027-591-1
; Sequence 1, Application US/10027591
; Patent No. US20020161014A1
; GENERAL INFORMATION:
; APPLICANT: SADDU, Chanchal et al.
; TITLE OF INVENTION: INHIBITORS OF HUMAN PHOSPHATIDYLINOSITOL 3-KINASE DELTA
; FILE REFERENCE: 27866/36170C
; CURRENT APPLICATION NUMBER: US/10/027,591
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/841,341
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/199,655
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 60/238,057
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent version 3.0
; SEQ ID NO 1
; LENGTH: 5220
; TYPE: DNA
; ORGANISM: Human p110delta complete cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (196)..(3327)
; US-10-027-591-1

Alignment Scores:
Pred. No.: 7,99e-111 Length: 5220
Score: 1033.00 Matches: 328
Percent Similarity: 43.76% Conservative: 194
Best Local Similarity: 27.49% Mismatches: 457
Query Match: 17.09% Indels: 214
DB: 9 Gaps: 41

US-08-908-453-1 (1-1146) x US-10-027-591-1 (1-5220)
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Db 202 CCTGGCGTGAAGCTGGCCCATGGAATTCGACCAAGAGAAATCAAGACCTT----- 255
QY 28 GluAsnGlyLysGlySerLeuLeuGluAsnGluGlyValAlaAspIleIleThrMet 47
Db 256 -----GTGGTGAACCTTC-----CTG 270
QY 48 CysProPheGlyGluValIleSerValAlaPheProTyrPheLeuAlaAsnValArgThr 67
Db 271 CTGCCCAAGAGGCTCACTCAAC-----TTCCCT-----GTG 303
QY 68 SerLeuGluIleLysLeuSerAspPheLysHisGlnLeu-----PheGlu 82
Db 304 TCCCGCAATGCCAACCTCAGCAACATCAAGAGCTGTGTGGACCGGCCGCAATGAG 363
QY 83 LeuIleAlaProMetLysTyrGlyThrTyrSerValLysProGlnAspTyrValPheArg 102
Db 364 CCGCTCTTCCACATGCTCAGTGGC-----CCGAGGCTATGTGTTCACC 408
QY 103 GlnLeuAsnAsnPheGlyGluIleGluValIlePheAsnAspAspGlnProLeuSerLys 122
Db 409 TGCATCAACCAAGACAGCGGACAGCAAGAGCTG-----GAGGACGACCAACGCGGTCTG 462
QY 123 LeuGluLeuHisGlyThrPheProMetLeuPheLeuTyrGlnProAspGlyIleAsnArg 142
Db 463 TGTGACGTGCAAGCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 522
QY 143 AspLysGluLeuMetSerAspIleSerHisCysLeuGlyTyrSerLeuAspLysLeuGlu 162
Db 523 AAGAAAGCTATCAACTCAAGATCAGCTCTCTCAATGCAAGAGGCTCCAGAGTTTGAC 582
QY 163 GluSerLeuAspGluGluLysLeuArgGlnPheArgAlaSerLeuTyrPheAlaArgThrLysLys 182
Db 583 TCCTTGTGCAAGCCAGAGAGTGAACGATTCGCGCAAGAGATGTCGAATTCGCAAGAG 642
QY 183 ThrCysLeuThrArg-----GlyLeuGluGlyThrSerHisTyrAlaPheProGlu 199

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Db	643	GC	GGCCCCGGCCGACAGCTGGGCTGGAGAGCCCTGGCTGCAGTACATTTCCCTCTG	702
Oy	200	GL	UINrYLeuCYsValGlyGluSerCYsProIysAspLeuGluSerLYsValLYsAla	219
Db	703	CAG	CTGGAGCCCTGGCTCAAACTGGGGGCTGTGATCCCTGGGCTCCGAACCGGGCC	762
Oy	220	Ala	LYsLeuSerTYrGluMetPheTrpArgLYsArgLYsAlaGluLYsGlyValCYs	239
Db	763	CTT	CTGTGCAAC-----GTTAATTGTAGAGGC---AGC	792
Oy	240	GLU	YSMetMetLYsILEGILlegluPheAsnProAsnGluThrProLYsSerLeuLeu	259
Db	793	GAG	GAGAGACTTCACCTTCCAGTG-----TCCACCAAGACGTGCCCTGGCTGTATG	846
Oy	260	His	TrPheLeuTYrGluMetArgLYsLeuAspValTYrAsp-----ThrAspAsp	276
Db	847	GCG	TGTGCGCTG-----CGGAAGAAGCCACAGTGTTCCGGACGCGCTGTGGAGCAG	900
Oy	277	Pro	AlaAspGluGlyTYrPheLeuGluLeuAlaGlyArgThrThrPheValThrAsnPro	296
Db	901	CCG	GAAGAC-----TACACGCTGGAGGTGAACCGCAGACGATGATCATCTGATGCG--	951
Oy	297	Asp	ValLYsLeuThrSerTYrAspGlyValArgSerGluLeuGluSerTYrArgCYsPro	316
Db	952	AAC	TACCCGCTCTGCGACGTTCCAGTACATCTGCACGCTGCCACAGTGGGTGACCTT	1011
Oy	317	Gly	PheValArgArgGlnSerLeuValLeu-----	327
Db	1012	CAC	CGACCATAGTGCATTTCTCTCCATTCCTCGGCAGCGGAGATGACAGAACACCT	1071
Oy	328	-----	LYsAspTYrCYsArgProLYsProLeuTYrGluProHisTYrVal	342
Db	1072	GCCCC	CCAGCTCCAGAAACCGCGTCCCAACCACTCCCATTT-----	1113
Oy	343	Arg	AlaHisGluArgLYsLeuAlaLeuAspValLeuSerValSerILEAspSerThrPro	362
Db	1113	-----	-----	1113
Oy	363	LYs	GlnSerLYsAsnSerAspMetValMetThrAspPheArgProThrAlaSerLeuLYs	382
Db	1114	-----	-----CTCGCAAGAGCCTTCC	1114
Oy	383	Gln	ValSerLeuTrpAspLeuAspAlaAsnLeuMetILEArgProValAsnILESerGly	402
Db	1132	TCT	GTGTCCCTGTGGTCCCTCGGACGAGCGTTCCCATCTGAG-----CTCATCAGAGGC	1185
Oy	403	Phe	AspPheProAlaAspValAspMetTYrValArgILEGluPheSerValTYrValGly	422
Db	1186	AGCAA	AGTGAACCGCAGCAGCGAGCGAGTGAAGCTGGTGTCAGAGCGCGGCTTTTCCACGGC	1245
Oy	423	Thr	LeuThrLeuAla-----SerLYsSerThrThrLYsValAsnAlaGluPheAlaIleTYrP	441
Db	1246	AAC	GAGATGCTGTGCAAGACGCTGCCAGCTCGAGAGTGAAGTCTCTCGGAGCCCTG	1305
Oy	442	Asn	LYsGluMetTYrThrPheAspLeuTYrMetLYsAspMetProProSerAlaValLeu	461
Db	1306	TGA	GAGCAGCGGCTGAGATTGCAATCAATCTCGACATCGCCCCGATGCGCGCTCTC	1365
Oy	462	Ser	IleArgValLeuTYrGly-----LYsVal	470
Db	1366	TGC	TTT-----GCGCTGTAGCGCTGTATGAGAAAGCAAGAGCTCGTCCACCAAGAG	1422
Oy	471	LYs	LeuLYsSerGluGluPheGluValGlyTYrValAsnMetSerLeuThrAspTrpArg	490
Db	1423	AAG	TCCAAAGAGCGGACTGCCCTTCCTGGCCAACTATGCTGTTGATCTACAAAG	1488
Oy	491	Asp	GluLeuArgGlnGlyGluPheLeuPheHisLeuTrpAlaProGluProThrAlaAsn	510
Db	1483	GAC	CCAGCTTAAGACCGGGGAACGCTGACATGTGGCCCTCGTCCAGATGAGAAG	1542
Oy	511	Arg	SerArgILEGlyGluAsnGly-----AlaArgILEGlyThrAsnAlaVal	527

Db 1543 GGCAGAGCTGCGAAACCCCAAGGGGACGTGTGGCAGTAAACCCCAACAGAGTAAAGCGCGCT 1602

Qy 528 ThrIle-----GluIleSerSerTyrGlyGlyArgValAlaGlyMetProSer 542

Db 1603 GCCCTGCTCATCTGCTCCCGAGGTGGCCCGCAC-----CCCGGTACTACCCCGCC 1656

Qy 543 GluGlyGlnTyrThrTyrLeuValAlaGlyHisArgSerThrTrpThrGluThrLeuAsnIle 562

Db 1657 CTGGAGAAGATCTTGGAGCTGGGGCGCAC----- 1686

Qy 563 MetGlyAspAspTyrGluSerCysIleArgAspProGlyTyrIleYsYsLeuGlnMet--- 581

Db 1687 -----ACGAGTGTGTGCATGTACACGAGGAGGACGCTGACGCTCGG 1731

Qy 582 ---LeuValIysYsYsIleGluSerGlyIleValIleGluGluAspGluGlnArgHisVal 600

Db 1732 GAAATCCTGGAGCGCGGGGGGTCTGGG---GAGCTGTATGACACGAGAAGACGACTGTGTG 1788

Qy 601 TrpMetTrpArgArgTyrIleGlnIysGlnGluProAspLeuLeuValLeuSerGlu 620

Db 1789 TGGAAAGCTGCGGACGTGAAGTCCAGAGACACTTCCCGAGGCGCTAGCCGCGCTGTG-- 1845

Qy 621 LeuAlaIleValTyrThrAspArgGluAsnPheserGluLeuYsYsValMetLeuGluYs 640

Db 1846 CTGTGTACCAAGTGAACAACAGCATGAGATGTGGCCAGATGCTCTACTCTGTGTCTCC 1905

Qy 641 TrpIysProProSerValAlaAlaAlaLeuThrLeuGluGlyIysArgCysThrAspArg 660

Db 1906 TGGCGGAGCTGCGCGCTCTGAGAGCGCCCTGAGCTGTACTACCTTCCCGATTCG 1965

Qy 661 ValIleArgYsPheAlaValGluYsLeuAsnGluIleuSerProValThrPheHis 680

Db 1966 CACGTAGGCTCTTGGCCATCAAGTCCGTCGGAACGTACGAGCATGAGCTGTTCAG 2025

Qy 681 LeuPheIleLeuProLeuIleGlnAlaLeuYsYsTyrGluProArgAlaGlnSerGluVal 700

Db 2026 ---TACTGCTGACGCTGTGTGACAGTCTCAAGTACAGTCTTACCTGACGTGAGCTG 2082

Qy 701 GlyMetMetLeuThrThrArgAlaLeuCysAspTyrArgIleGlyHisArgLeuPheTyr 720

Db 2083 ACCAAATTCCTGCTGACCGGGCCCTGGCCAAACCGCAAGATCGGCCACTTCTTTCTGG 2142

Qy 721 LeuLeuArgAlaGluIleAlaArgLeuArgAspCysAspLeuYsSerGluGluTyrArg 740

Db 2143 CACCTCGGCTCCGAGATG---CACGTCCCGCTGGTGCCCTG----- 2181

Qy 741 ArgIleSerLeuMetGlnAlaTyrLeuArgYsAsnGluGlnHisIleYsIle 760

Db 2182 CGCTTCGGCTCTCATCTCGAGGCTTACTGCAAGGCGACAGCACCAACATGMAAGTCTG 2241

Qy 761 ThrArgIleValAspMetValAspGluLeuThrArgIleSerThrLeuVal----- 777

Db 2242 ATGAAGACAGGGGANAAGCATGAGCAAACTGAAGCCCTGATGACTTCGTCAAGCTGAGC 2301

Qy 778 -----LysGlyMetProLysAspValAlaThrMetYsLeuArgAspGlu 792

Db 2302 TCTCAGAGAACCCCAAGCCCAACACCAAGAGCTGATGACCTTGTCATGACGCGCACAGAG 2361

Qy 793 -----LeuArgSerIleSerHisIleMetGluAsnMetAspSerProLeuAspProVal 810

Db 2362 GCCTAACTAGAGCGCTCTCCAC-----CTGCACTCCCACTGACCCACAGC 2409

Qy 811 TyrIleLeuGluGluMetIleIleAspIysAlaIleValIleGluGlnSerAlaYsArgPro 830

Db 2410 ACCCTGCTGGCTGAAGTCTGCTGGAGACAGTGCACCTTACATGACTCCAAAGATGAACCC 2469

Qy 831 LeuMetLeuHisTrpIlyAsnIlyAsnProLysSerAspLeuIleValProPheCysAla 850

Db 2470 CTGTGATCATGATCACCAACGAGAGGACAGGACGCGCGCAAGCTG-----GGC 2520

Qy 851 MetIlePheYsAsnGlyAspAspLeuArgIleAspMetLeuValLeuGlnIleValGlu 870

Db 2521 ATCATCTTTAAGACGGGAGTGAACCTCCGGAGGACATGCTGACCTGTCAATATATCCAG 2580

[illegible]

Db	1594	TCGAAAGCTGGGGCATGAAATCTCAGAGACATCTCCGGAGCGCTAGCCCGAGCTGCTG---	1650
Oy	621	LeuAlaPheValTTPthTAspArgGluAsnPheserGluLeuTyrValMetLeuGluLys	640
Db	1651	CTGATCTACCAAGTGGAAACAAAGCATGAGAGATGTGGCCAGAGCTCTACCTCTGTGCTCC	1710
Oy	641	TrpLysPProPserValAlaAlaAlaLeuThrLeuLeuGlyLysArgCysThrAspArg	660
Db	1711	TGGCCGAGAGCTGCCCGCTCTGAGGGCCCTGGAGCTGTAGCTTACGTTCCAGTCCCGATGTC	1770
Oy	661	ValIleArgLysPheAlaValAlaGluLysLeuAsnGluLeuSerProValThrPheHis	680
Db	1771	CAGGTAAAGCTCTTGGCATCAAGTCGTGGGAAATGACGAGCATGATGATCTGTTCCAG	1830
Oy	681	LeuPheIleLeuPProLeuIleGlnAlaLeuLysTyrGluProArgAlaGlnSerGluVal	700
Db	1831	---TACCTGCTGCAGCTGTGTGCAGGTGTCTCAATGACGATCCGCTGAGCTGCAGCTG	1887
Oy	701	GlyMetMetLeuLeuThrArgAlaLeuCysAspArgTyrArgIleGlyHisArgLeuPheTrp	720
Db	1888	ACCAAAATTCCTGCTGAGACCGGGCCCTGGCCCAACGCAAGATGGCCATCTCTTTCTCG	1944
Oy	721	LeuLeuArgAlaGluIleAlaArgLeuArgAspCysAspLeuLysSerGluGluTyrArg	740
Db	1948	CACCTCCGCTCCGAGATG---CAGTGGCGCTGGAGCGCTG-----	1986
Oy	741	ArgIleSerLeuLeuMetGluAlaTyrTyrLeuArgGlyAsnGluGluHisTyrLeuIleLe	760
Db	1987	CGCTTCGGCTCATCTCTGAGAGGCTCTACGTGACGGGAGGAGACCCACCATATAGAGTGTCTG	2046
Oy	761	ThrArgGlnValAspMetValAspGluLeuThrArgIleSerThrLeuVal-----	777
Db	2047	ATGAGACAGGGGGAGGACATGAGCAAACTGAAAGCCCTGAATGACTTGTCAAGCTGAC	2106
Oy	778	-----LysGlyMetProLysAspValAlaThrMetLysLeuArgAspGlu	792
Db	2107	TCTCAGAAAGACCCCAAGCCCCCAACAGAGAGCTGATGCACTTGTGATGGGAGAG	2166
Oy	793	-----LeuArgSerIleSerHisLysMetGluAsnMetAspSerProLeuAspProVal	810
Db	2167	GCTTAACCTAAGAGGCGCTCTCCAC-----CTGCAGTCCCACTGCAGCCCAAGC	2214
Oy	811	TyrLysLeuGlyGluMetIleIleAspLysAlaIleValLeuGlySerAlaLysArgPro	830
Db	2215	ACCCGTGCTGAGTCTGCTGAGTCTGCTGAGGACGACCTTCAATGACTCCAAATGAAAGCCC	2277
Oy	831	LeuMetLeuHisTTrpLysAsnLysAsnProLysSerAspLeuHisLeuProPheCysAla	850
Db	2275	CTGTGAGATCATGTACGACACGAGAGGACGAGCGGCGGCGGACGCTG-----GGC	2322
Oy	851	MetIlePheLysAsnGlyAspAspLeuArgGlnAspMetLeuValLeuGlnValLeuGlu	870
Db	2326	ATCATCTTTAAGAACGGGGATGACTCCGCGACAGCATGTGACCTCTCAGATGATCAG	2385
Oy	871	ValMetAspAsnIleTTrpLysAlaAlaAsnIleAspCysLysLeuAsnProTyrAlaVal	890
Db	2386	CTCATGACGCTCTGTGTGACGACGAGGGGTGACTGTGAGATACACCCCTATATGGCTGC	2445
Oy	891	LeuProMetGlyGluMetIleGlyIleTleGluValValProAsnCysLeuThrIlePhe	910
Db	2446	CTCCCAACCGGGAGCCGACAGGCTCTATTGAGGTGTACTCCGTTCCAGACACATCCGC	2500
Oy	911	GluIleGlnValGlyThrGlyPheMetAsnThrAlaValArgSerIleAspProSerPhe	930
Db	2506	AACATCAACTCAACAAAGACAAATG---GAAGCCACAGCGCGCTTCAACAAAGATGCC	2565
Oy	931	MetAsnLysTTrpIleArgLysGlnCysGlyIleGluAspGluLysLysLysSerLysLys	950
Db	2563	CTGCTCAACTGTGCTGAG-----	2580
Oy	951	AspSerThrLysAsnProIleGluLysLysIleAspAsnThrGlnAlaMetLysLysTyr	970

QY 420 -----TyrValGlyThrLeuThr 426
 Db 1786 CACAGACTACAAAGCATTTTCATTTCTCTGCTGCATCATATGCTGGAAAGAGCTGT 1845
 QY 426 euAlaSerIysSer-----ThrThylsValAsnAlaGlnPheAlaLysT 441
 Db 1846 GCCAAGTAAAGCTGCAGATCCCTGCCAGTCAAAAGCATCTTCTTTTGGGGAAGT 1905
 QY 441 rPAsnLysGluMetYrThrPheAspLeuTywMetLysAspMetProPheSerAlaValL 461
 Db 1906 GGAAT---GAAATATCAATTTTCTTGCATTAAGTCAAGTCTCCAAAGATCATCATGC 1962
 QY 461 euSerIleArgValLeuTyrglyLysValLysLeuLysSerGluGlnPheGluValGlyT 481
 Db 1963 TCGTATATAAG---CTGTTTGGATTGACAGTGCACCCACAGCCGAAATCTGCGCCT 2019
 QY 481 rPValAsnMetSerLeuThrAspTrpArgAspGluLeuArgGlnGlnPheLeuPheN 501
 Db 2020 GGACCTGCTTCACATATTT----- 2039
 QY 501 iLeuTrpAlaProGluProThrAlaAsnArgSerArgIleGlyGluAsnGlyAlaArgI 521
 Db 2040 -----CCAAAAGAAAGCTCCGCTGGGGTCTAGAGCTTCTCAGCA 2079
 QY 521 IeGlyThrAsnAlaAlaValThrIleGluIleSerSerYrGly-----GlyArgV 538
 Db 2080 TTAACACTACAGAGTGCCTCTATAGAAATAGTGCCTCAGAGATGATGGATGGAGGCC 2139
 QY 538 aArgMetProSerGlnGlyGlnTyrThrTyreValLysHisArgSerThrTrp--- 556
 Db 2140 ACCCTAACCCACAGACCCGACATAGATTT-----CCAGTGCACCTGGGAGT 2190
 QY 557 -----ThrGluThrLeuAsnIleMetGlyAspAspTyrglu-----SerCysI 571
 Db 2191 AGCTGAACCTGACACTGAAGAAAGAACTGACCAAGAGGCTCCCAAGAGAGTGT 2250
 QY 571 IaArgAspProGlyTyrglyLysLysLeuGlnMetLeuValLysLysHisGluSerGlyIleV 591
 Db 2251 TA-----AAACACATGCGACAGACTCTCCCAAAAG---CAGCTCCCTTCC 2292
 QY 591 aIleGluGlnLysArgGlnGlnArgHisValTrpMetTrpArgTyrglyIleGlnLysGlnG 611
 Db 2293 TACTTCTCTGGAAGAGAGAGATATTGTGCTTTATGCTTCTCTGCAACAAGAGAGA 2352
 QY 611 LysProAspLeuLeuIleValLeuSerGluLeuAlaPheValTrpThrAspArgGluAsn 631
 Db 2353 ACTCTCTCTCTCCCTCTGCTCTGGGAGC---GCCCTGCTGG---GATGAAGGAGCAG 2406
 QY 631 heSerGluLeuTyrglyValMetLeuGlnLysTrpLysProPheSerValAlaAlaLeuT 651
 Db 2407 TTTTGGAAATGCAAGCCGCTTGAGAAAGGAGCATTTTCCATCCGTTGGAAGCTCTTG 2466
 QY 651 hTrLeuLeuGlyLysArgCysThrAspArgValIleArgLysPheAlaValGluLysLeuA 671
 Db 2467 GCCTTTTGACTTCCAGGTTTCCAGACCAAGACATTTGTGAAGTTGGCGTTCAACACTTG 2526
 QY 671 snGluGlnLeuSerProValThrPheHisLeuPheLeuPro---LeuIleGlnAlaL 690
 Db 2527 ACAACTCTTGAACCGATGAGCTG---CTGAGCTGCTCCACAGCTAGTTCAGGCTG 2580
 QY 690 euLysTyrgluProArgAlaGlnSerGluValAlaGlyMetLeuLeuThrArgAlaLeuC 710
 Db 2581 TCAAGTTTGAAGTGAAGTCTGAAAGTCCCTTGATGAGACTCCGCTTTCATCGATCTTGC 2640
 QY 710 yAspTyrglyArgIleGlyHisArgLeuPheTrpLeuLeuArgAlaGluIleAlaArgLeuA 730
 Db 2641 AAAGACTCGAGTGGCTCACCGCTGTCTGCTGCTGCG--- 2681
 QY 730 rAspCysAspLeuLysSerGluGlnTyrglyArgIle-----SerLeuLeuMetC 747
 Db 2682 -----GATGACAAAGGTGAAGACTATTAAAGCTGCTACAGAGACTTTTGGCGC 2733

QY 747 LuAlaTyrglyLeuArgGlyLysGlnGluHisIleLysIleIleThrArgGlnValAspMetV 767
 Db 2734 CTCTCAGATTCTGTGCAGAGAAAGCCCTGATCGAAGAGCTTCCAAAGCAGAAACTTG 2793
 QY 767 aLAspGluLeuThrArgIleSerThrLeuLysV-----GlyMetProLysA 783
 Db 2794 TCAACTCCTCGGGTGATATTGAGAAAGAGTGGCGCTGCGATGCTCAGAGAAAGG 2853
 QY 783 sPValAlaThrMetLysLeuArgAspGluLeuArgSerIleSerHisLysMetGluAsnM 803
 Db 2854 ATGTG-----CTAAAGAGAGATTGGCAGTCTAGAGAAATCTTTAAAGATA 2901
 QY 803 eAspSer-----ProLeuAspProValTyrglyLysGlyGluMetIleLeuAspL 820
 Db 2902 TTAAGACTTGCATCTTCTCTGAACCCGCGCTGCTGCTAAAGAGATTGACGGAGTG 2961
 QY 820 yAlaAlaLeuValLeuGlySerAlaLysArgProLeuMetLeuHisTrpLysAsnLysAsn 840
 Db 2962 CATGTCATATTTCATCTTAATGCGCTTGCCATTAAGATCATCTTCATCAATGCTTAATC 3021
 QY 840 rOlySerAspLeuHisIleuProPheCysAlaMetIlePheLysAsnGlyAspAspLeuA 860
 Db 3022 CAATGGC-----AAAAATATCAGGTATATTTTAAAGCCGCGCAGATCTTC 3069
 QY 860 rGlnAspMetLeuValLeuGlnValLeuGluValMetAspAsnIleTrpLysAlaAlaA 880
 Db 3070 GGCAGATATGCTTCTTCTGAGATTAATCAAGTATAGCAACCTTGGCTTCAGAGAG 3129
 QY 880 snIleAspCysAspLeuAsnProTyrglyAlaValLeuProMetGlyGluMetIleGlyIleI 900
 Db 3130 GCCTGATATGCAATGATCATTTATGATGCTGACCAAGAGAAAGCTCAGAGATTCA 3189
 QY 900 IeGluValValProAsnGlyLysTrpIlePheGluIleGlnValGlyThrGlyPheMetA 920
 Db 3190 TAGAGATGCTGCTATGATCTGTAAAGCTTGGCCAAATCATTTGACTGCGCTG--- 3245
 QY 920 snThrAlaValArgSerIleAspProSerPheMetAsnLysTrpIleArgLysGlnCysG 940
 Db 3246 -----ATAGAGACCCCTGAAAGAAACACCATCAAGAGTGTTC----- 3284
 QY 940 LylIleGluAspGluLysLysLysSerLysLysAspSerThrLysAsnProIleGluLysL 960
 Db 3285 -----AGTCAGACCAACCATTAAGAGAGATTGAAAGG 3321
 QY 960 ySIIeAspAsnThrGlnAlaMetLysLysTyrglyPheGluSerValAspArgPheLeuTyrs 980
 Db 3322 CCTGAGGAAAC-----TTTTTTACT 3342
 QY 980 eFCysValGlyTyrglySerValAlaThrTyrglyMetGlyIleLysAspArgHisSerAspA 1000
 Db 3343 CTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3402
 QY 1000 snLeuMetLeuThrGluAspGlyLysTyrglyHisIleAspPheGlyHisIleLeuGlyN 1020
 Db 3403 ATATCATGCTGCAAAAGTCAAGGCGCCACATGTTTCATATTGACTTGAATAATCTTGGGTC 3462
 QY 1020 iLeGlyLysThrLysLeuGlyIleGlnArgAspArgGlnProPheIleLeuThr----- 1037
 Db 3463 AGCACAACCATTTGGCGGTATATAAAGGAGCGGCGCTTCAATTTTACTTTCAGAGA 3522
 QY 1038 --GluHisPheMetThrValIleArgSerGlyLysSerValAspGlyAsnSerHisGluL 1057
 Db 3523 TGGAGTACTTTATTCG-----GAGCGTGGGAA-----AACACAGAGCATT 3564
 QY 1057 euGlnLysPheLysThrLeuCysValGluAlaTyrglyGluValMetTrpAsnAsnArgAspL 1077
 Db 3565 TTCAGACTTCTGGAACCTCTGTCAGAGCTTAACAACATTTGTGAGGAAGCAGACCAAC 3624
 QY 1077 euPheValSerLeuPheThrLeuMetLeuGlyMetGluLeuProGluLeuSerThrLysA 1097
 Db 3625 TCTCTGAGCTTCTTGAAGAAAGATGCTGATGCCGCGCTTCTTCAAGCTGAGAGGGGATGG 3684
 QY 1097 IaAspLeuAspHisLeuLysLysTrpLeuPheCysAsnGlyGluLysSerGluGluAlaA 1117

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Db      3665 AAGACCTGAATAACCTACACGCAATCTCCGGCCCAAGACACAGACCTGGAAGCCACA 3744
Qy      1117 rglvPhePheAaIlelyIleTyrglu-----gluAlaPheAenIleTyrsPseTrrL 1135
Db      3745 GTCATTTTACCAAGAGATTAAGACAGACTGTGAGTGGCTTC-----CCAGTTA 3792
Qy      1135 ysthrAsenTrrleupPheHisAlaVal 1143
Db      3793 AACTGAATTAACCTGATTCACAGCGCTT 3818

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RESULT 6

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US-10-092-219-1
; Sequence 1, Application US/10092219
; Patent No. US20020115114A1
; GENERAL INFORMATION:
; APPLICANT: Domin, Jan
; TITLE OF INVENTION: No. US20020115114A1 Lipid Kinase
; FILE REFERENCE: 1064HG/50947
; CURRENT APPLICATION NUMBER: US/10/092,219
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: PCT/GB98/00244
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/355,160
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 9701652.1
; PRIOR FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5061
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(5058)
; OTHER INFORMATION:
US-10-092-219-1

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Alignment Scores:

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Pred. No.: 2.07e-62 Length: 5061
Score: 624.00 Matches: 207
Percent Similarity: 45.44% Conservative: 122
Best Local Similarity: 28.59% Mismatches: 301
Query Match: 10.32% Indels: 94
DB: 12 Gaps: 24

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US-08-908-453-1 (1-1146) x US-10-092-219-1 (1-5061)

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Qy      440 LysTrrPheNlySGlMetTyThrPheAsePleuTyrmElyAsePmeProPseRala 459
Db      2218 AAATGGAT--GAACCTAATCTTTTCTTCTATCCAGATATTCACAATGGCCATTAGAAATCA 2274
Qy      460 ValLeuSerIleArgValLeuTyrglyLysVal----- 470
Db      2275 GTTCTTCACTT--ACTCTTTTGGAAATTTAAATCAGACAGCGAAGTTCCCTGAT 2331
Qy      471 -----LysLeuLysSerGluGluPheGluValGlyTrrPValAsmEseSerIleThrAsp 488
Db      2332 TCTAATAAGCAGAGAAAGGAGACAGAGACTTTGGCAAGTTCTTTACCTCTTTGTGAC 2391
Qy      489 TrrPArgPgluLeuArgGlnIyGlnPheLeuPheHisLeuTrrAlaProGluProThr 508
Db      2392 TTTAGACGGTTTAAACATGCGAAGCTTAACCTTCTAATCTTTGAGACTTCATCACAATACA 2451
Qy      509 AlaAsenArgSerArgIleGlyGluAsnGlyAlaArgIleGlyThrAsnAlaAlaValThr 528
Db      2452 -----AATCTGTTCCGGAACGTTACCAAAAAGGA 2484
Qy      559 IleguIleSerSerTyrglyIyArgValAlaGmeCProSerGlnGlnIyThrTyrr 548
Db      2485 TATGTATGAGAAAGATATGTCTGCTACAGGATTTTCTTCTCCCT-----GCATTT 2535

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Qy      549 LeuVallySHisArgSerThrTrrPheGluThrIleuAsnIleMeGlyAAspArgIyrglu 568
Db      2556 GATATTATTATTAACACTCCCTCAAGTTGACAGAGACATTTATACAGACATTAATCAAGTA 2595
Qy      569 SerCySileArgAspProGlyTyrrLyLysLeuGlnMetLeuVallySHisIleGluSer 588
Db      2596 ACACAGAGAAATGATATTAAGGAGAACTCTGATATTCCTTCAATAAA-----GACTCA 2649
Qy      589 GlyIleValLeuGluAspGluGlnArgHisValTrrPmeTrrPArgTyrrIleGln 608
Db      2650 TCATCTGACCTTCTTAAGAAAGATTAACCTTTTATGAGAG--AAACGTTATTAATTCG 2706
Qy      609 LysGlnGluProAspLeu-----IleValLeuSerGluLeuAlaPheValTrrThr 626
Db      2707 TTCAAAACCCAAATATGCTTCTTAAATATTTAGACAGCCGCCAACTGAAATGCG--- 2763
Qy      627 AspArgGluAsnPheSerGluLeuTyrrValMetLeuGluTyrrTyrrPseProPseRala 646
Db      2764 -----GGTAATCTTGCAGAAACCTTACATGCTTCCACAGTGGCTGCATTTGACCA 2817
Qy      647 AlaAlaAlaLeuThrIleuGlyIyArgGlySerThrAspArgValIleArgLysPheAla 666
Db      2818 CTAAATGCAATGGAACTTCTTGATTCAAATTTGCTGATCAGAGTAAGATCCCTAGCT 2877
Qy      667 ValGluLysLeuAsnGluGlnLeuSerProValThrPheHisLeuPheIleuProLeu 686
Db      2878 GTGACCTGGATT--GAGGCCATTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2934
Qy      687 IleguAlaLeuLysTyrgluProArgAlaGlnSerGluValGlyMeuMetLeuLeuThr 706
Db      2935 GTACAGCTTTGAAATATGAATGAATTTACTGAAATGATTCATTAATGCAATTCCTTTGACC 2994
Qy      707 ArgAlaLeuCyAspTyrrArgIleGlyHisArgLeuPheTrrPleuLeuArgAlaIle 726
Db      2995 AGGGCATTGGGAAATATCCAGATGACACAAATTAATATGCTTCTCAAA----- 3045
Qy      727 AlaArgLeuArgAspCyAspLeuLysSerGluGluTyrrArgArgIle-----SerLeu 744
Db      3046 GATGCCCTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3102
Qy      745 LeuMetGluAlaTyrrLeuArgGlyAsnGluGlnHisIleLysIleIleThrArgGlnVal 764
Db      3103 CTGTGACGAGGAGGAGAAAGCACTTAGAGAGAACTTCAAAA-----CAGACG 3150
Qy      765 AspMetValAspGluLeuThrArgIleSerThrLeuValLys-----GlyMetPro 781
Db      3151 AAACCTGTACAGCTTTTAGAGAGATGACAGAAAAAGTAAGCAGAGCTAGTGAACAGCC 3210
Qy      782 LysAspValAlaThrMetLysLeuArgAspGluLeuArgSerIleSerHisLysMetGlu 801
Db      3211 AGACAGGTTGTTCCCAAGAGATGAGACGATGACAGCTCTTTTCAAGAA---AAT 3267
Qy      802 AsnMetAspSerProLeuAspProValTyrrLysLeuGlyGluMetIleIleAspLysAla 821
Db      3268 AAATGCCCTCCCTCCCTCAAGCAAGCTAGTGGCAAAAGATTAATTAATTAATTAATTAAT 3327
Qy      822 IleValLeuGlySerAlaLysArgProLeuMetLeuHisIleTrrPseAsnLysAsnProLys 841
Db      3328 TCCTTCTTCACTTGAATGCTGCTGCTCCCTTAAGCAATAGTGAATGCTGACCTCTG 3387
Qy      842 SerAspLeuHisLeuProPheCyAlaMetIlePheLysAsnGlyAspAspLeuArgGln 861
Db      3388 GGAGAA-----GAAATTAATGCTAGTTTAAAGTTGAGTTGAGAACTTCTGCGAA 3435
Qy      862 AspMetLeuValLeuGlnValLeuGlnValMetAspAsnIleTrrPseAlaAlaAsnIle 881
Db      3436 GATATGTTAGCTTTAAGATGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 3495
Qy      882 AspCySylAsnProTyrrAlaValLeuProMetGlyGluMetIleGlyIleIleGlu 901
Db      3496 GATCTGAGAGATGATTAATTAATTAATGCTTCAACTGCGACAGATCGAGGATGCTGAG 3555
Qy      902 ValValProAsnCyLysThrIlePheGluIleGlnValGlyThrGlyPheMetAsnThr 921

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QY 592 -----LeuGluGluAspGluGlnArgHis 599
 DB 1086 CTACAAACATATTAAAGTTTCCTCCTACAGCACCTGGAGAGTGAAGAGCAATTG 1145
 QY 600 ValTyrMetTyrPargArgTyrIleGluGluGluProAspLeuLeuIleValLeuSer 619
 DB 1146 GTGTGAAGATTTCGTTCTCTCTTGTGCTGAGAAAGAAAGCTTCAACGAAATTTGTCGC 1205
 QY 620 GluLeuIleAspValTyrThrAspArgGluAsnPheserGluLeuTyrValMetLeuGlu 639
 DB 1206 TCAGTGAGT-----TGAAGTATTAACCAAGAGCTTAAGCAAGCTGTGAGTGAATGGA 1259
 QY 640 LysTyrLysProProSerValAlaAlaIleThrLeuGluGlyAspCysThrAsp 659
 DB 1260 AAGTGGAAATGATGATGATGCTGATGACCTAGAGCTTCTCTCAGCTGATTTGAAAGC 1319
 QY 660 ArgValIleArgLysPheAlaValGluLysLeuAsnGluGlnLeuSerProValThrPhe 679
 DB 1320 GACGAAAGTTCGGTATGCTGTCTGACGCACTT---GAAAGGGCTGATGATGAATTA 1376
 QY 680 HisLeuPheIleLeuProLeuIleGlnAlaLeuLysTyrGluProArgAlaGlnSerGlu 699
 DB 1377 CAGTGTATTTATCTCAGTTAGTGAAGCTTTCGTTGAAAGATCTGACAGATCCGCT 1436
 QY 700 ValGlyMetMetLeuLeuThrArgAlaLeuCysAspTyrArgIleGlyHisArgLeuPhe 719
 DB 1437 CTAGCACTCTTCTTGTAAACCGTCTTGTCTCAACATCGAAATTCGTAAGTCTCTCCG 1496
 QY 720 TrpLeuLeuArgAlaGluIleAlaArgLeuArgAspCysAspLeuLysSerGluLysTyr 739
 DB 1497 TGTATATATATTAGTTAGT---CTTCACAGTCTCTCAATAT 1532
 QY 740 ArgArg-----IleSerLeuLeuMetGluAlaTyrLeuArg----- 751
 DB 1533 GCAGAACCATATTATGACACATATGACATGCTTGAACACAGATGATGAATGCTTGCT 1592
 QY 752 -----GlyAsnGluGluHisIleLysIle-----IleThrArgGlnValAsp 765
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 DB 1692 AATGTAAGAGTAGCGCCACAAAGAAATTTGAAATTAAGGACACTATATTCACAGAGTT 1751
 QY 797 SerHisLysMetGluAsnMetAsp-----SerProLeuAspProValTyrLys 812
 DB 1752 TTCAGTGAAGCTTACAACTTTGATGAGCCAAATGCTTTCACCACTTTCACCAAGCTTCTC 1811
 QY 813 LeuGlyGluMetIleIleAspLysAlaIleValLeuGlySerAlaLysArgProLeuMet 832
 DB 1812 CTACAGAGAGTGTGCTCAAGAAATCGTCTATATTAAGAGGAGCTTGAACCTTTGGCGC 1871
 QY 833 LeuHisTyrLysAsnLysAsnProLysSerAspLeuHisLeuProPheCysAlaMetIle 852
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 QY 853 PheLysAsnGlyAspAspLeuArgGlnAspMetLeuValLeuGlnValLeuGluValMet 872
 DB 1914 TACAAAAGAGGTGATGACCTCCGCAAGATCAGTTTATTCAAACGTTCTTGTGATG 1973
 QY 873 AspAsnIleTyrLysAlaAlaAsnIleAspCysCysLeuAsnProTyrAlaValLeuPro 892
 DB 1974 GACCACCACTCAATTAAGAAATCTAGATTTCGACCTTACCTCAACGAGTTCTTCCA 2033
 QY 893 MetGlyGluMetIleGlyIleIleGluValAlaProAsn-----CysLysThrIle 909
 DB 2034 ACTGACAAAGATGAAGGAGTGTAAATTTATTAAGTTCCAGTCTCTTGGACAGATTTCTA 2093
 QY 910 PheGluIleGlnValGlyThrGlyPheMetAsnThrAlaValArgSerIleAspProSer 929

DB 2094 TCAGAAACATCCAGATATTACAAAGTTTACCTACAGAAAGTTCCATCMTGATGAGATGCTCT 2153
 QY 930 PheMetAsnLysTyrIleArgLysGlnCysGlyIleGluAspGluLysLysLysSerLys 949
 DB 2154 TTT-----GGTATTAACGGCTCAAGT----- 2174
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 DB 2538 GAGAAATTCGCGTTGGAGTCTGAC----- 2561
 QY 1113 LysGluGluAlaArgLysPhePheAlaGlyIleTyrGluGluAla 1127
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 US-09-921-330-1
 ; Sequence 1, Application US/09921330
 ; Patent No. US20020102682A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Martino-Calc, Susan J.
 ; APPLICANT: Wang, Hongyu
 ; APPLICANT: Beach, Larry R.
 ; TITLE OF INVENTION: Polypeptides Controlling Phyate
 ; TITLE OF INVENTION: Metabolism in Plants
 ; FILE REFERENCE: 070603
 ; CURRENT APPLICATION NUMBER: US/09/921,330
 ; CURRENT FILING DATE: 2001-08-02
 ; PRIOR APPLICATION NUMBER: 60/055,446
 ; PRIOR FILING DATE: 1997-08-11
 ; PRIOR APPLICATION NUMBER: 60/055,526
 ; PRIOR FILING DATE: 1997-08-08
 ; PRIOR APPLICATION NUMBER: 60/053,944
 ; PRIOR FILING DATE: 1997-07-28
 ; PRIOR APPLICATION NUMBER: 09/118,442
 ; PRIOR FILING DATE: 1998-07-17
 ; PRIOR APPLICATION NUMBER: 09/677,064
 ; PRIOR FILING DATE: 2000-09-29
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1

; LENGTH: 3252
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (258) ... (2666)
 ; NAME/KEY: misc feature
 ; LOCATION: (1) ... (3252)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-921-330-1

Alignment Scores:

Pred. No.:	3, 71e-54	Length:	3252
Score:	551.50	Matches:	200
Percent Similarity:	38.68%	Conservative:	123
Best Local Similarity:	23.95%	Mismatches:	297
Query Match:	9.12%	Indels:	215
DB:	10	Gaps:	27

US-08-908-453-1 (1-1146) x US-09-921-330-1 (1-3252)

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QY 415 IlegluPheSerValTyValglYThrLeuThrLeuAlaSerLysSerThrThrLysVal 434
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QY 435 AsnAlaGlnPheAlaLys-----TTPAsnLysGluMetTyThrPheAspLeuTyMet 452
DB 441 GAACCTTTCGACCGCAAAATACGTGTGAAT---GAGCTCATATACATTAAGTACCAATAC 497
QY 453 LysAspMetProProSerAlaValLeuSerLeArgValLeuTyrgLysValLysLeu 472
DB 498 AGGAGCTTAACATCCCTCTCGACGCTTGCAATTAAGGTG-----TGGAGATGCTCATCT 551
QY 473 LysSerGluGluPheGluValglYTrpValAsnMetSerLeuThrAspTrpArgSerGlu 492
DB 552 GGTGGAACCTGAGGTTGTGCGTGAGCCACCATTCTTTTTCACAGCAAAAGGCGAG 611
QY 493 LeuArgGlnGluPheLeuPheHisLeuTrpAlaProGlu----- 506
DB 612 CTTAAACAGAAAGACAGAAAGCTCGCGCTGTGCCCCACAAAGAGGAGCATGAGAGATC 671
QY 507 ProThrAlaAsnArgSerArgLlegLysGluAsnGlyAla----- 519
DB 672 CCACACACAACCTCGGCAAGGTTCTAGGAATGAGAGGGGTGATAGACGTTTGAA 731
QY 520 ----- 520
DB 732 AGGCTTGAACAGATGAGAGAGGAGGAGATACACATGTTGCTTATCTCTT 791
QY 522 GlyThrAsnAla----- 525
DB 792 GCCTTCAGTGTATGACAAAGCTATGCAAAAAGAGTGTGAGAGGAGCCCAATTTGTAC 851
QY 526 ---AlaValThrLlegLysSerSerTyrgLysArgValArgMetProSerGlnGly 544
DB 852 CCGAGCTGTGTGATGATGAGTTCGAAATGCGAATGATGCTTCCAGGATCTGGA 911
QY 545 GlnTyThrTyLeuValLysHisArgSerThrTrpThrGluThrLeuAsnLleMetGly 564
DB 912 GCAAATTTTATACACCGGCCCGAGTATCATTAACAATGAACTGCTTACTGTATG--- 968
QY 565 AspAspTyrgLysSerCysLleArgAspProGlyTyTrpLysLysLeuGlnMetLeuValLys 584
DB 969 ---GACCTCGAAGTTGGAAAGAACCAATCCATCTGACACAGCATTAAGCTTGCTAG 1025
QY 585 LysHisLeuSerGlyLleVal----- 591
DB 1026 AGCTTACCTCGGAGATGATGTATAGATCTTAAACCAAGCTCAATGAGAGAAGTTA 1085
QY 592 ----- 592
DB 1086 CTACAAACAATATTATTAAGTTCTCTACACGCACTGTGAAAGTGTGATGAGAGCAATTG 1145
  
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QY 620 GluLeuAlaPheValTrpThrAspArgGluAsnPheSerGluLeuTyValMetLeuGlu 639
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QY 660 ArgValLleArgLysPheAlaValglYLysLeuAsnGlnGlnLeuSerProValThrPhe 679
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DB 1437 CTAGCACTCTTCTTGTAAACCGTGTGTGTCACATGCAAAATGCTTACGCTTCTCCG 1496
QY 720 TrpLeuLeuArgAlaGluLleAlaArgLeuArgAspCysAspLeuLysSerGluGluTy 739
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DB 1533 GCAAGACATATTTATGCAATATGACATGCTGTGAAAACAGTATGATCAATTTGTTGCT 1592
QY 752 -----GlyAsnGluGlnHisLleLysLle-----LleThrArgLleValAsp 765
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QY 786 ThrMet-----LysLeuArgAspGluLeuArgSerLle 796
DB 1692 AATGTAAAGTAGGAGCACAAGAAATGAAATGAAATGAGGACACTTATTCACAGAGTT 1751
QY 797 SerHisLysMetGluAsnMetAsp-----SerProLeuAspProValTyrgLys 812
DB 1752 TTCAGTGAAGCTTACAACTTGTATGAGCAATTCCTTACCACTTATGCAACCACTTCTC 1811
QY 813 LeuGlyGluMetLleLleAspLysAlaLleValLeuGlnGlySerAlaLysArgProLeuMet 832
DB 1812 CTAAAGAGATGTGTCTCCAAAGATCGTCTATATTAGAGAGTGTGACCTTGACCTTTGGCG 1871
QY 833 LeuHisTrpLysAsnLysAsnProLysSerAspLeuHisLeuProPheCysAlaMetLle 852
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DB 1914 TACAAAGAGGTGATGACCTCGGCAAGATGATGTTGTTATTCACAAAGGTTTCTTTGATG 1973
QY 873 AspAsnLleTrpLysAlaAlaAsnLleAspCysLysLeuAsnProTyrgLleValLeuPro 892
DB 1974 GACCACTACTCAATTTAGAAAATTTAGATTTGACACTTACTCCATACGAGTTCTTGCA 2033
QY 893 MetGlyGluMetLleGlyLleLlegLysValAlaProAsn-----CysLysThrLle 909
DB 2034 ACTGACAAAGATGAGGAGTGTGAATTTATTTAGTTCAGATTCTCTTGACAGATTTCTA 2093
QY 910 PheGlnLleGlnValglYThrGlyPheMetAsnThrAlaValArgSerLleAspProSer 929
DB 2094 TCAGAACATCGCAGATTTACCAAGTTTACCTACAGAAAGTTTCATCMTGATGAGAGATGCTCT 2153
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Qy      970 TyrPheGluSerValAspArgPheLeuTyrSerCysValGlyTyrSerValAlaThrTyr 989
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Qy      990 IleMetGlyLysLysAspArgHisSerAspAsnLeuMetLeuThrGlnAspGlyLysTyr 1009
Db      2223 ATATTGGGGGTTGAGACACAGCATCTGATATCTTCTTCACTGATGATGAGCGCTT 2282
Qy      1010 ValHisIleAspPheGlyHisIleLeuGlyHisGlyLysThrLysLeuGlyIleGlnArg 1029
Db      2283 TTTCATGTGTGACTTTTGTCTTTATCTTGG-----CGA 2315
Qy      1030 AsparGlnProPhe-----IleLeuThrGlnHisPheMetThrValIle 1044
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Qy      1085 MetLeuGlyMetGluLeuProGluLeuSerThr-----1095
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Qy      1113 LysGluGluAlaArgLysPhePheAlaGlyIleTyrGluGluAla 1127
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RESULT 9
US-09-921-329-1
; Sequence 1, Application US/09921329
; Patent No. US20020110884A1
; GENERAL INFORMATION:
; APPLICANT: Martino-Catt, Susan J.
; APPLICANT: Wang, Hongyu
; APPLICANT: Beach, Larry R.
; TITLE OF INVENTION: Polypeptides Controlling Phytate
; FILE REFERENCE: 0706D2
; CURRENT APPLICATION NUMBER: US/09/921,329
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/055,446
; PRIOR FILING DATE: 1997-08-11
; PRIOR APPLICATION NUMBER: 60/055,526
; PRIOR FILING DATE: 1997-08-08
; PRIOR APPLICATION NUMBER: 60/053,944
; PRIOR FILING DATE: 1997-07-28
; PRIOR APPLICATION NUMBER: 09/118,442
; PRIOR FILING DATE: 1998-07-17
; PRIOR APPLICATION NUMBER: 09/677,064
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3252
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:

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; NAME/KEY: CDS
; LOCATION: (258)...(2666)
; NAME/KEY: misc_feature
; LOCATION: (1)...(3252)
; OTHER INFORMATION: n = A,T,C or G
US-09-921-329-1

Alignment Scores:
Pred. No.: 3,71e-54 Length: 3252
Score: 551.50 Matches: 200
Percent Similarity: 38.68% Conservative: 123
Best Local Similarity: 23.95% Mismatches: 297
Query Match: 9.12% Indels: 215
DB: 10 Gaps: 27

US-08-908-453-1 (1-1146) x US-09-921-329-1 (1-3252)
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Qy      435 AsnAlaGlnPheAlaLys-----TrpAsnLysGluMetTyrThrPheAspLeuTyrMet 452
Db      441 GAACCTTCTGACCGCAAAATACGTGTGGAT--GAGCTCATACATTAAGTACCAAAATAC 497
Qy      453 LysAspMetProPheSerValValLeuSerIleArgValLeuTyrGlyLysValLysLeu 472
Db      498 AGGAGCTCAATACATCCCTCTCGAGCTTGCATTTACGGTG-----TGGAGTCTCATCT 551
Qy      473 LysSerGluGluPheGluValGlyTyrValAsnMetSerLeuThrAspTrpArgAspGlu 492
Db      552 GGTGAGAACCTGAGGTTGTGCTGGTGAGCCACCATTTCTTTTAAACAGCAAAAGGACG 611
Qy      493 LeuArgGlnGlyGlnPheLeuPheHisLeuTrpAlaProGlu-----506
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Db 1812 CTACACGAGATGTGCTCCTCAAGATGCTATATTTAAAGATGCTTGAACCTTTGGCCG 1871
QY 833 LeuHisIleTrpLysAsnLysAsnProLysSerAspLeuHisLeuProPheCysAlaMetIle 852
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QY 893 MetGlyLysMetIleGlyIleIleGlnValValProAsn-----CysLysThrIle 909
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QY 910 PheGlnIleGlnValAlaLysThrGlyPheMetAsnThrAlaValArgSerIleAspProSer 929
Db 2094 TCAGAACATCGCAGTTTACAGATTAACAGAGTACAGAGATGATGATGATGATGCTCT 2153
QY 930 PheMetAsnLysTrpLysArgLysGlyIleGlnAspGluLysLysSerLys 949
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QY 950 LysAspSerThrLysAsnProIleGluLysLysIleAspAsnThrGlnAlaMetLysLys 969

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QY 990 IleMetGlyIleLysAspArgHisSerAspAsnLeuMetLeuThrGlnAspGlyLysTyr 1009
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QY 1045 ArgSerGlyLysSerValAspGlyAsnSerHisGluLeuGlnLysPheLysThrLeuCys 1064
Db 2370 ATGGGTGGT-----GCAGAAAGCCATTTTACACAGAGTTCAAGTCTTACTGC 2417
QY 1065 ValGlnAlaTyrGluValMetTrpAsnAsnArgAspLeuPheValSerLeuPheThrLeu 1084
Db 2418 TGGAGAGCATACAAATCTCTGAGAGAGTCCAGAGCTTCATTTGAATCTAATCAAGCTG 2477
QY 1085 MetLeuGlyMetGluLeuProGluLeuSerThr----- 1095
Db 2478 ATGGAGCGATCAGGATTCGCGACATCTCTGCGATGAAGCGAGGCTTCAAGCTCAG 2537
QY 1096 -----LysAlaAspLeuAspHisLeuLysLysThrLeuPheCysAsnGlyLysSer 1112
Db 2538 GAGAAATTCGGTGTGATGATGAC----- 2561
QY 1113 LysGluGlnAlaArgLysPhePheAlaGlyIleTyrGluGlnAla 1127
Db 2562 GACGAGAGGCGTATACATTTCTTCCAGATCTTATCAACGATAGC 2606

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RESULT 10

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US-09-771-161A-10
; Sequence 10, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 2418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-771-161A-10

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Alignment Scores:

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Pred. No.: 2,566-36 Length: 2418
Score: 399.00 Matches: 175
Percent Similarity: 35.59% Conservative: 114
Best Local Similarity: 21.55% Mismatches: 261
Query Match: 6,60% Indels: 262
DB: 10 Gaps: 30

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US-08-908-453-1 (1-1146) x US-09-771-161A-10 (1-2418)

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Qy 388 AspleuAspAlaAsnLeuMetIleArg----- 396
Db 87 GACCTGATATCAACGCTCAGCTTAAGACAGAGCTGGAAAGGAGAGACAAAG 146
Qy 397 -----ProValaAsnIleSerGlyPheAspPheProAla 407
Db 147 AGTTATAAAGCTGTCCTGGAGACCCAAATGTCTCAGAGCTATATACAGAGACA 206
Qy 408 AspValaAspMetTyrValArgIleGluPheSerValTyrValGlyThreLeuThrLeuAla 427
Db 207 TGCTGTGATCTTATGTTACTTGTCTCAA-----GTTTTGCAGAAAGGAGACCTTTGGCC 260
Qy 428 SerLysSerThrThrLysValaAsnIleGluPheAlaLysTyrAsn---LysGluMetTyr 446
Db 261 TTGCAGAGAGAACATCTCACAAGACATTTATACAAAGATGGAATCGAATGAATGAGCGCTG 320
Qy 447 ThrPheAspLeuTyrMetLysAspMetProProSerAlaValLeuSerIleArgVal--- 465
Db 321 AAACACAGAGTAAATACCTGACCTGCCAGGAATGCCCCAAGTGCCTTACACCATATGG 380
Qy 466 ---LeuTyrGlyLysValLysLeuLysSerGluGluPheGluValGlyTyrValaAsnMet 484
Db 381 GATGTGATGGTCCCGGAAA-----GCAGTCCCTGTAGAGAGAAACAACGGTT 428
Qy 485 SerLeuThrAspTyrPArgAspGluLeuArgGlnGlyPheLeuPheHisLeuTyr--- 503
Db 429 TCGCTCTTGGAAATACGGCATGTTTCCCAAGGAGTGCATGACTTGAAACTGCGCT 488
Qy 504 -----AlaProGluProThrAlaAsnArgSerArgIleGlyLysGlnGly 518
Db 489 AATGAGACAGATGATGATCAGAACCCCAAAAACCTCCGCGACA----- 533
Qy 519 AlaArgIleGlyThrAsnAlaAlaValThrIleGluIleSerSerTyrGlyValArgVal 538
Db 534 -----ACAGTAGCACTCTCTCAGAAAGATCAGATGACCGCTCTTGGC 575
Qy 539 ArgMetProSerGlnGlyInTyrThrTyrLeuValLys-----HisArgSer 554
Db 576 AAGCTCACCAAGATCATGACACAGAGACATGATGGAAGTAGATTGGCTGATGATTGG 635
Qy 555 ThrTyrThrGluThr-----LeuAsn 561
Db 636 ACATTTAAGAAATAGAAATGATAATAGAGCTGCAAAAGATTCTAATTCATGTAC 695
Qy 562 IleMetGly-----AspAsp-----Tyr 567
Db 666 CTGATGGGCGATTTGATGATGTCAGATGTCATGATAGAAATATGATTTGTTATAT 755
Qy 568 GluSer-----CysIleArg 572
Db 756 GAAAGACACGATGATCATCTCCAAATTTTAAACAATTGATGTAAGTTCTCT 815
Qy 573 AspProGlyTyrLysLysLeuGlnMetLeuValLysValHisGluSer----- 588
Db 816 GACCCCGAGATGTCCTGGAGAAATTTAGTTGAGACAAACACCAACCTTCCCGAGT 875
Qy 588 ----- 588
Db 876 TTAAAGAGTGAACCTTTCAGACCAAGATCTGAACCTATCTTCCCGAGAGATCAGTTA 935
Qy 589 ---GlyIleValLeu-----GluGluAspGluGlnArgHisVal 600
Db 936 AAAAATATTTGATGATTCCTTCATCCCAAGCAACCAACATATAGAACAAATCTGT 995
Qy 601 TrpMetTyrPArgArgTyrIleGlnLysGlnGluProAspLeuLeuIleValLeuSerGlu 620
Db 996 TGGGATTTAGATATTTACTTACGATCAAGATTAAGCCTTGACCAAAATCTCTGACATCT 1055
Qy 621 LeuAlaPheValTyrThrAspArgLysPheSerGluLeuTyrValMetLeuGluLys 640
Db 1056 GTT-----ATTGGATCTACCTCAGGGGGCCAAACGGCTTGACATTTTGGGAAA 1109
Qy 641 TrpLysProProSerValAlaAlaLeuThrLeuLeuGlyLysArgCysThrAspArg 660

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Db 1110 TGAACCCGATGATGATGAGAGACTCTTGGAGCTGATATCTCTCATTTACCAACCA 1169
Qy 661 ValIleArgLysPheAlaValGlyLysLeuGlnGluInLeuSerProValThrPheHis 680
Db 1170 ACTGGAGCCGTTATGCTGTGGCCGGTTG---GCACAGGCCGATGATGAGATTTGTTG 1226
Qy 681 LeuPheIleLeuProLeuIleGlnAlaLeuLysTyrGlu----- 693
Db 1227 ATGTACTTATTCATTTGGTCCAGGCTCTCAAAATGTGAAATTTTGATGATTAAGAAT 1286
Qy 693 ----- 693
Db 1287 GGATTGAACCTACCAAGAGATAGTCAGAGTTCAGTGTGCAAAATGTGCAATTTCT 1346
Qy 693 ----- 693
Db 1347 GGAAATTAATTCGAGAAATAGATAGCTCCAAATTAATACAGCCCTTCTCAGTC 1406
Qy 694 -----ProArgAla-----GlnSer 698
Db 1407 TCTTACCTCTCTCTGCTACAAAACAAAGAGTTCCAGATGGGAAATCTGAAACA 1466
Qy 699 GluValGlyMetMetLeuLeuThrArgAlaLeuCysAspTyrArgIleGlyHisArgLeu 718
Db 1467 GATCTCTGATCTTCTTATATCGAGAGCTGCAAAAACCTCAACCTGGCTAATATTATTA 1526
Qy 719 PheTyrP-----LeuLeuArgAlaGluIleAlaArgLeuArgAspLeuLysSer 736
Db 1527 TACTGTATGTGATGTGGAATGTGAAATGATCAAGATACCTCAGCAGAGATCCAAAGACC 1586
Qy 737 GluGlu-----TyrArgArgIleSerLeuMetGluAlaTyrLeuArg 751
Db 1587 CATGAGATGACTTCAACGTATAGCAATTCAC-----CAAGCATTTGTTGAAG 1637
Qy 752 GlyAsnGluGlu-----HisLeuLysIleIleThrArgGlnValaAspMetValAsp 768
Db 1638 GGTGATTAAGTGTGTCAGAGTTATGCGTTCTTGGCGTGACACACAGCATTTGTAAGT 1697
Qy 769 GluLeuThrArgIleSerThrLeuValLysGlyMetProLysAspValAlaThrMetLys 788
Db 1698 CCGTGTGTGCAT-----CTAATGAAGGACATCAACCGGAAGTGAATGCTAAG 1748
Qy 789 LeuArgAspGlu-----LeuArgSerIleSerHisLysMet----- 800
Db 1749 AAAAGAAATGAGACTACAGGCAATTCCTGGAGATTAATGAAGATGATTTGTCAGAT 1808
Qy 801 ---GluAsnMetAspSerProLeuAspProValTyrLysLeuGlyGluMetIleIleAsp 819
Db 1809 GTGGAATTAATCCGTCCTGCTTTAGAACCCCAAGGAAATATAGAGAAATATTCGCGAA 1868
Qy 820 LysAlaIleValLeuGlySerAlaLysArgProLeuMetLeuHisTyrLys----- 836
Db 1869 ACAGCTACACGTTTAAAGTCCCTTATGCTGCACAGTTGTTTAAAGCGAGAGAT 1928
Qy 837 ---AsnLysAsnProLysSerAspLeuHisLeuProPheCysAlaMetIlePheLysAsn 855
Db 1929 GAGGCAAAATATCA-----GTTATATTATTAAGAT 1958
Qy 856 GlyAspAspLeuArgGlnAspMetLeuValLeuGlnValaLeuGluValaMetAspAsnIle 875
Db 1959 GGAAGATTAATTCGTCAGATCAACTTATCTTCAAAATCATTTCACTGACACAAGCTG 2018
Qy 876 TrpLysAlaAlaAsnIleAspCysLeuAsnProTyrAlaValaLeuProMetGlyGlu 895
Db 2019 TTACGAAAGAAATCTGCACTTGAAATTTGACACCTTATTAAGTGTGTCACCAAGTACA 2078
Qy 896 MetIleGlyIleIleGluValaValaProAsnGlySerThrIlePheGluIleGlnValaGly 915
Db 2079 AAACATGCTTATGCAAGTTATTCAGATGAT---CTGTGGCTGAAGTTTGTATATACA 2135
Qy 916 ThrGlyPheMetAsnThrAlaValaArgSerIleAspProSerPheMetAsnLysTyrIle 935

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Qy 871 ValMetAspAsnIleThrLysAlaIleAsnIleAspCysCysLeuAsnProTyrAlaVal 890
   ::::::::::::::::::::
Db 4990 CTAATTAGAACATTGGTCTAGTATGGCTGAGATGCTAGGTTTCCCTACAGAGT 5049
Qy 891 LeuProMetGlyGluMetIleGlyIleIleGluValProAsnCysLysThrIlePhe 910
   ::::::::::::::::::::
Db 5050 ACTGGACGGACCGCGGTGGTGGTCATCGATGCTCCCAAT-----TCGGATCC 5103
Qy 911 GluIleGluValIleThrGlyPheMetAsnThrAlaValAspSerIleAspProSerPhe 930
   ::::::::::::::::::::
Db 5104 CGTGAATGATTGGA-----CGTGAAGCTGTAATGAATGATATATGAAATTTTC 5151
Qy 931 MetAsnLysThrIleArgLysGlnCysGlyIleGluAspLulLysLysSerLysLys 950
   ::::::::::::::::::::
Db 5152 ACTAGTAATTT----- 5163
Qy 951 AspSerThrLysAsnProIleGluLysLysIleAspAsnThrGlnAlaMetLysLysTyr 970
   ::::::::::::::::::::
Db 5164 -----GGTAAAGAACTCTACTATCGAATTT 5187
Qy 971 PheGluSerValAspArgPheLeuTyrSerCysValIleTyrSerValAlaThrTyrIle 990
   ::::::::::::::::::::
Db 5188 CAATAACGACGCAACCACTTGTAAATCTTAGCGGATATAGCGTAATTTGCGATTTGG 5247
Qy 991 MetGlyIleLysAspArgHisSerAspAsnLeuMetLeuThrGluAspGlyLysTyrVal 1010
   ::::::::::::::::::::
Db 5248 TTGCAATTCAGATGATGACATATAGTAACTTATGTCAGATGATCAAGACATTTGCTCA 5307
Qy 1011 HisIleAspPheGlyHisIleLeu-----GlyHisGlyLysThrLysLeuGly 1026
   ::::::::::::::::::::
Db 5308 CATATCGATTTGGGTTTATTTTGTATATTTGCCAGGT-----GGT 5349
Qy 1027 IleGluAspArgGlnProPheIleLeuThrGluHisPheMetThrValIleArgSer 1046
   ::::::::::::::::::::
Db 5350 ATCAAGTTTGAAGCGATACCATTTCAAGCTGACGAAAGAAATGCTTAAAGTATG----- 5403
Qy 1047 GlyLysSerValAspGlyAsnSerHisGluLeuGln-----LysPheLysThrLeu 1063
   ::::::::::::::::::::
Db 5404 -----GGAGGTTCCGCCACGACCCGACCGCTATCTGGACTTGAAGAACTT 5448
Qy 1064 CysValGluAlaIleTyrGluValMetTyrPheAsnAsnArgAspLeuPheValSerLeuPheThr 1083
   ::::::::::::::::::::
Db 5449 TGTATCAAGGCGATCTAGCCGCCGCTCCGACGTCGAGCCATATATGATGCTGAAT 5508
Qy 1084 LeuMetLeuGluLysMetGluLeuProGluLeuSerThrLysAlaAspLeuAspHisLeuLys 1103
   ::::::::::::::::::::
Db 5509 CCTATGTTAGGAAGCGGCTCTCCCTGCTTAAAGGCTCACAGACATTTAGGAATCTAAGA 5568
Qy 1104 LysThrLeuPheCysAsnGlyLysLeuSerLysGluGluAla----- 1116
   ::::::::::::::::::::
Db 5569 GCAAGATTTCACACCTCAAAAAACGATCGACGACGCTCATATATGAGCGCTAATC 5628
Qy 1117 ArgLysPhePheAlaGlyIleTyrGluGluAlaPheAsn 1129
   ::::::::::::::::::::
Db 5629 CGTAAAGTTATGAAGTATATTCTCACTAAGGTTATGAT 5667

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RESULT 12

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US-09-925-302-205
; Sequence 205, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 205

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; LENGTH: 2620
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (563)
; OTHER INFORMATION: n equals a,t,c,g, or c
; NAME/KEY: misc feature
; LOCATION: (1838)
; OTHER INFORMATION: n equals a,t,c,g, or c
; NAME/KEY: misc feature
; LOCATION: (2596)
; OTHER INFORMATION: n equals a,t,c,g, or c
; NAME/KEY: misc feature
; LOCATION: (2609)
; OTHER INFORMATION: n equals a,t,c,g, or c
US-09-925-302-205

Alignment Scores:
Pred. No.: 1.34e-25
Score: 309.00
Percent Similarity: 33.46%
Best Local Similarity: 21.14%
Query Match: 5.11%
DB: 10 Gaps: 46

US-08-908-453-1 (1-1146) x US-09-925-302-205 (1-2620)

Qy 129 PheProMetLeuPheLeuTyrGlnProAsp---GlyIleAsnArgAspLysGluLeuMet 147
   ::::::::::::::::::::
Db 39 TTCAGATTAATGTTCTGCTACTTGTAGATTAAGCTAATTCAGAAACAAA----- 89
Qy 148 SerAspIleSerHisCysLeuGlyLysTyrSerLeuAspLysLeuGlnSerLeu----- 165
   ::::::::::::::::::::
Db 90 TCTGGATGATGACAGTGTGTGATTCAGCTCCGCGCAAAAGTATTCGATCCTTCTGTAAC 149
Qy 166 -----AaPGluGluLeuArgGlnPheArgAla 174
   ::::::::::::::::::::
Db 150 ATGATGCGCGATTAAGCCAAAGCAAGCAAGAAAGCAAGAGACGCTGAGCGGACGTCAG 209
Qy 175 SerLeuTyrPheAlaArgThrLysLysThrCysLeuThrArgGlyLeuGlnGly-----Thr 192
   ::::::::::::::::::::
Db 210 TCTCTGTGGTGAACCTCA-----ACCACATCCACAAAGAGATTAAGAGGTTGGCAGACA 263
Qy 193 SerHisTyr-----AlaPheProGluGluGlnTyrLeuCysValGly-Gl 207
   ::::::::::::::::::::
Db 264 AGTATCTATCTGCTGCTGCTGATAGATTTCCTCC-----ACTTGCTCTGAGAGG 311
Qy 207 userCysProLysAsp-LeuGluSerLysValLysAlaLysLeuSerTyrGlnMetP 227
   ::::::::::::::::::::
Db 312 GGACTGTGCTGAAGCAATCTGTCGACATCTGACACACCTGTCACTGTCTACTG----- 364
Qy 227 heTPArgLysArgLysAlaGluIleAsnGlyValCysGluLysMetMetLysIleGlnI 247
   ::::::::::::::::::::
Db 365 -----AGCCTGATATTTCAC-----AAGATATCAGC 389
Qy 247 IeGluPheAsnProAsnGluThrProLysSerLeuLeuHisThrPheLeuTyrGluMetA 267
   ::::::::::::::::::::
Db 390 CTTACTATGACATCCCGACGCGCCCTACCGGATCAGGTTCTCTGACACGTAAGAGCCG 449
Qy 267 rGlyLeuAspValTyrAspThrAspAspProAlaAspGluGlyTyrPheLeuGlnLeuA 287
   ::::::::::::::::::::
Db 450 GTGAAGACATTTG-----AAGAGCTTCGCTGACACGCTGTGGATGATCTCTCCAGAG 503
Qy 287 IeGlyArgThrThrPheValThrAsnProAspValLysLeuThrSerTyrAspGlyValA 307
   ::::::::::::::::::::
Db 504 CCATGAAGTGGCA-----CTTACGCTC-----ACCA 530
Qy 307 rGSerGluLeuGluSerTyr-----ArgC 315
   ::::::::::::::::::::
Db 531 AGTCCACCTCGAGGAATCTGAAACAACATNAGACTGGGTATCGGAGCTGCTCCAGC 590
Qy 315 yEPProGlyPheValArgArgGlnSerLeuValLeuLysAspTyrCysArgProLysP 335

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Db 591 AACAGGGGCTGGCCATGGCCACTGAGACATCCTT----- 625
 Qy 335 roleuylrgluprohietyrvalargalhielgluargylsleualaleuaspvalleus 355
 Db 626 -----CACTTGCTGGCTACACAGACAGACAACTTGGGGCAATC 671
 Qy 355 eValSerlleasberthrrpolsnglnserlysaenserapmetValmetthrAsp 375
 Db 672 ACCTAGC-----G 680
 Qy 375 hArgProthrAlaSerleuylsGlnValSerleuThrAspLeuaspAlaAsnleuMetI 395
 Db 681 ACCGGCCGGCCCTGTGAGAGAAAGACTACTCCAACTTCATGGATCCCGATCTCGCGA 740
 Qy 395 lArgProValAsnilleSerlyPheAspPheProAlaAspValAspMetIyryValArgI 415
 Db 741 ACCGCTACCGGGGAC-----GAGGTGATGGAATGA 770
 Qy 415 lgluPheSerValIyryValglYThrleuThrleuAlaSerlySerThrThrIys--V 434
 Db 771 TTCGTTCTTCAGGCACACAGCCAGATGTGACCTGAACAAATGATGTCCAGGATC 830
 Qy 434 aAlaAsnIaglnPheAlaIySTrPAsnlySgluMetIyThrPheAspLeuIyry----- 451
 Db 831 TACATTCAGCTTAGACCCGACATCCTCAGACATCACAGCGCATCTTCAGCTGA 890
 Qy 452 -----MetIyAspMetProProSerAlaValleuSerlleArgValI 466
 Db 891 CCGCAATGCTCATTAGCAGTAAAGATTGACCCG----- 925
 Qy 466 eutYrclYrlyVallylsleuylsSerclgluPhegluValglYTrPValAsnMetSerI 486
 Db 925 ----- 925
 Qy 486 eutThrAspTrpArgAspGluLeuArgGlnIyGlnPheLeuPhehiSleu---TrpAlaP 505
 Db 926 -----CAGCTCCTTCATCATCTGTGCTGGGGTC 953
 Qy 505 rogluProthrAlaAsnArgSerArgIleGlyGluAsnGlyAlaArgIleGlyThrAsnA 525
 Db 954 CCGT-CCGATGTTCATGACGATGACATGACAGACCCCTGCTGGAGTGGCTG 1012
 Qy 525 lAlaValThrIleGluIleSerSerIyGlyIyArgValArgMetProSerGlnGlyG 545
 Db 1013 CTGGC-----TGGCAAGATGAGTGAAGTGC--GTTCCGTG 1050
 Qy 545 lntYrThrIyLeuValIyShIsArgSerThrTrpThrIgluThrleuAsnIleMetGlyA 565
 Db 1051 -----CACCTGGACACACATCGA----- 1068
 Qy 565 sPAspTrpIgluSerCySilleArgAspProGlyTyryIySlySleuGlnMetLeuVallyuI 585
 Db 1069 -----CGCCGATC----- 1077
 Qy 585 yshIeSgluSerGlylleValleuGluGluAspGlnGlnArgIshIValItrpMetTrpArgA 605
 Db 1078 -----TCAGAGCTCAGCCATGTGCTGTGCTGG--- 1104
 Qy 605 rGlyrIleGlnIySnglnIuProAspLeuLeuIleValleuSerGluLeuAlaPheValI 625
 Db 1105 -----GCGGCCACGACACACCC----- 1122
 Qy 625 rPThrAspArgIgluAsnPheSerGluLeuTyryValIleuGluIySTrPlyAspPropros 645
 Db 1123 --ACAGGCTCTCTCTCTCTCAGCATGAC-----CCGCGCG 1159
 Qy 645 eValAlaAlaAlaIleuThrleuGluIySArgCyThrAspArgValIleArglyAsp 665
 Db 1160 ACCCTTCACGGGCG-----CAGTACGGGGTGAAGTCTTCGGGCTC 1201
 Qy 665 heAlaValaIgluylsleuAsnGluGlnleuSerProValThrPhehiSleuPheIleuP 685
 Db ----- 685

Db 1202 TC-----CCTCGGACGGCATCCTCTTMTACATCCCC 1234
 Qy 685 roleuIleGlnAlaLeuylsTyryGluProArgAlaGlnSerGluValaIgluMetleuL 705
 Db 1235 AGATTGTACAGCCCTCAGTACGAC-----AAGATGGCTTATGTGGAGATATATTC 1288
 Qy 705 eutThrArgAlaLeuCyAspTrpArgIleGlyIySArgLeuPheThrleuAspArgAlaG 725
 Db 1289 TGTGGCAGCGCTTAATCCACAGCTTGTGGACACCATTCATCTGAAACATGAAGACTA 1348
 Qy 725 lulle-----AlaArgleuArgAspCyAspLeuylsSerGluIyryA 740
 Db 1349 ACATTATTCATGATGAGAGGGCCACAGAAAGACCTGACATCGCGCAC----- 1398
 Qy 740 rGArgIleSerleuLeuMetGlu-----AlaTyrleuArgglYanGluGlnhiS 757
 Db 1399 --CTCTGATCAGTGTGTGATGAGAGATCACAGGCTCTGTGCCGCCAGCAAG--- 1452
 Qy 757 lelyIleIlethrArglnValaAspMetValaAspGluLeuThrArgIleSerThrleuV 777
 Db 1453 --GACTTTACAGCGGAGATTGTATTCTTAACAAGATCACCAAGCTGTGGCTATCA 1510
 Qy 777 aIlySglYMetProIyAspValaAlaThrMetIySleuArgAspGluLeuArgSer--- 795
 Db 1511 TCAAGCCCTACCTTAAGGC-----GACGAGAGAAAGAGGCTT 1549
 Qy 796 --IleSerhiSlyMetGluAsnMetAspSerPro----- 806
 Db 1550 GTCTGTGCGCCCTGTCTGAAGTGAAGTGACGCCGCTGCTCTGCCAGCAACCTTG 1609
 Qy 807 -----LeuAspProValIyryIys-LeuGly----- 814
 Db 1610 AAGCATTTGTGTGAACRTCACTCAATCAAGTCTGGACCCCATGAGAGTGTGCAGAAAG 1669
 Qy 815 -----GluMetIleIleAspIyAlaIle 822
 Db 1670 CCCCATATCTGCGCAAGTTCAAGTGAAGCATGTGAGTTGATGAACTTGAAAAAGAG 1729
 Qy 823 ValIleGlySerAlaIlyArgProleuMetleuhiSTrPlyAsnIyAsnProIySser 842
 Db 1730 GTCTCGGGTGGCGCTCAGACTCCGAGAGTGCAGACGACGAGAGGCCGACGACAGA 1789
 Qy 843 AspLeuhiSleuProPheCyS-AlaMetIlePheIySAsnGlyAspAspLeuArgIlnAs 862
 Db 1790 GATTC-----CTGGCAGGACCCATCTTCAAGTGGAGAGACGACTGCGGACAGA 1840
 Qy 862 pMetleuValleuGlnValleuGlnValMetAspAsnIleTrpIyAlaAlaAsnIleAs 882
 Db 1841 CATGCTGGCCCTGCAGATCATGACCTCTTCAAGAACATCTTCCAGCTGTGCGGCTGGA 1900
 Qy 882 pCySlySleuAsnProIyryAlaValleuProMetGlyGluMetIleGlyIleIleGluVa 902
 Db 1901 CCTCTTTGTTTTCCTTACCGGCTGTGAGCCACTGCCCTGGGTGGGTATGAGAGTG 1960
 Qy 902 lValProAsnCySlyThrIlePheGluIleGlnValaIglYrGlyPheMetAsnThrAl 922
 Db 1961 CATCCCACTGACCTCCCGGACACAGTGGCCGCGACAGACACTT----- 2009
 Qy 922 aValArgSerIleAspProSerPheMetAsnIySTrPleArgIyGlnCyGlyIleG 942
 Db 2010 -----GCGATGACACTACTTACACACCCGACTACGGG----- 2042
 Qy 942 uAspGluylslySserlySleuAspSerThrIyAsnProIleGluIylySleIleAs 962
 Db 2043 -GATGAGTCACACTGCGCTTCACAGAGGCCGCTACAC----- 2081
 Qy 962 pAsnThrGlnAlaMetIySlySTrPheGluSerValaAspArgPheLeuTySerCySya 982
 Db 2082 -----TTCATCCAGACATGCG 2098
 Qy 982 lglYrSerValaAlaThrTyryIleMetGlyIleIySAspArgIshIsAspAsnleuMe 1002
 Db 2099 CGCTACAGCCTCTGCTGTCTGCTGCTGATCAAGGACAGACACAAAGCAACATTAAT 2158

Db 2278 -----AAGAAAGCTACAGCT 2294
 QY 950 sAspSerThrlYsAsnProIleGluLysLysIleAspAsnTrgAlaIleMetLysLysTy 970
 Db 2295 CTCCTTGCTCGATTCTTCTTACAGAG-----CAGCGCATTTACACCACTAGAGCATT 2348
 QY 970 rHeGluSerValAspArgPheLeuTySerCysValGlyTySerValAlaThrTyr11 990
 Db 2349 CCTCAGTCACAGCCGCAATTTGTGCAAGTTGTGTGGTGTCTGCTGTCTTACT 2408
 QY 990 eMetGlyLysIleAspArgHisSerAspAsnLeuMetLeuTrgAlaSPGlyLysTyVal 1010
 Db 2409 GCTGCAAGTCAGACAGACAGACAGATTCCTTTGAGCGCAAGAGGCATCAT 2468
 QY 1010 HisIleAspPheGlyHisIleLeuGlyHisGlyLysTrpLysLeuGlyIleGlnArg 1030
 Db 2469 CCACATCGACTTGGCTTCATCTCTCCAGCTCACCCCGAAATCTGGGCTTT-----GA 2522
 QY 1030 pArgGlnProPheIleLeuThrGlnHisPheMetTrpAlaIleArgSerGlyLysSerVal 1050
 Db 2523 GAGCTCAGCTTTAAGCTATACACAGAGTTTGTGATGTGATG-----GGCGGCT 2573
 QY 1050 IAspGlyAsnSerHisGluLeuGlnLysPheLysTrpLeuCysValGluAlaTyArgGluVal 1070
 Db 2574 GGATGGCCGACATG-----TTCACTACTATAAGATCGTATGCTGCAAGGGCTGATTGC 2627
 QY 1070 IMetTrpAsnAsnArgAspLeuPheValSerLeuPheTrpLeuMet--LeuGlyMetG1 1089
 Db 2628 CCCTCGAAACACATGACAGAGTGTGCGAGATCGTGCAGATCATCTACCAAGGTTCTCA 2687
 QY 1089 uLeuProGluLeuSerThrlYsAlaAspLeuAspHisIleLysLysTrpLeuPheCysAs 1109
 Db 2688 GCTCTCTCTCTTCATGCTGCTCCAGACCAATTCGAAACCTCAAGAGAGAG-----TTCCACAT 2744
 QY 1109 nGlyGluSerLysGluGluAlaArgLysPhePheAlaGlyIleTyGluGluAlaPheAs 1129
 Db 2745 GAGCATGACTGAGAGGACACTGACGCTG-----CTGGTCAGACAGATGTGTGA 2792
 QY 1129 nGlySerTrpSerThrlYsTrpAsnTrpLeuPheHisAlaValLysHis 1145
 Db 2793 TGGCAGTATGCGGTCTATGACCAACCAACTATGACGCGCTTCAGTAC 2841
 RESULT 14
 US-09-976-165-29
 ; Sequence 29, Application US/09976165
 ; Patent No. US20020107383A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FUJIMURA, TSUTOMU
 ; APPLICANT: WATANABE, TAKESHI
 ; APPLICANT: HORIE, MASANO
 ; TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
 ; TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONUGATING ENZYME
 ; FILE REFERENCE: Q-53599
 ; CURRENT APPLICATION NUMBER: US/09/976,165
 ; PRIOR FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/565,538
 ; PRIOR FILING DATE: 2000-05-05
 ; PRIOR APPLICATION NUMBER: 09/055,699
 ; PRIOR FILING DATE: 1998-04-07
 ; PRIOR APPLICATION NUMBER: 08/820,170
 ; PRIOR FILING DATE: 1997-03-19
 ; PRIOR APPLICATION NUMBER: JP 63410/1996
 ; PRIOR FILING DATE: 1996-03-19
 ; PRIOR APPLICATION NUMBER: JP 69163/1997
 ; PRIOR FILING DATE: 1997-03-05
 ; NUMBER OF SEQ ID NOS: 95
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 29
 ; LENGTH: 2451
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-976-165-29

Alignment Scores:
 Pred. No.: 1,5e-19 Length: 2451
 Score: 257.50 Matches: 131
 Percent Similarity: 39.87% Conservative: 107
 Best Local Similarity: 21.94% Mismatches: 239
 Query Match: 4.26% Indels: 122
 DB: 10 Gaps: 26
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 Db 869 AACGAAACGCCAGCAACCTTAAGTGAATGAGATGAGAGAGCTCTCTCCAGCACCG 928
 QY 613 AspLeuLeuIleValLeuSerGluLeuAlaPheValTrpTrpAspArgGluAsnPheSer 632
 Db 929 AGAGTATGATTAATTCATTTCAGTTCCCTGTTCAGCTGCTCTCCAGAGAAATTCATCA 988
 QY 633 GluLeuTyTrpValMetLeuGluLysTrpLysProPheSerValAlaAlaLeuThrLeu 652
 Db 989 AGT-----CCCTGATGGCGATCGGCAACCGG-CTGGCCAGCTCCCCACC 1032
 QY 653 LeuGlyLysArgCysTrpAspArgValIleArgLysPheAlaValGluLysLeuAsnGlu 672
 Db 1033 AAAGAGCAGAAA--ACACAGAGGCTGATCTCAGAGCTCTCCCTG-----CTCAACAT 1083
 QY 673 GlnLeu-----SerProValTrpPheHisLeuPheIleLeu 684
 Db 1084 AAGCTCCCTGCCAGTGTGCTGCCACTCTGCTTTGACACACAGTGTGTGCTGTGA 1143
 QY 685 ProLeuIleGlnAla-LeuLysTyTrpArgTrgArgLagIn----- 697
 Db 1144 CCCACACACAGGCTGTGTCTCTCACTCCAGACAGCAAGGCTCCCTACTGATTATGTG 1203
 QY 698 -SerGluValGlyMetLeuLeuThrArgAlaLeuCysAspTyArgIleGlyHisArg 717
 Db 1204 GAAGTCTTGAATGTGAACCTTTCACACACACAGAGTTC-CTGCGCGAGATCCCGAGAA 1262
 QY 717 GluPheTrpLeuLeuAlaGluIleAlaArgLeuArgAspCysAspLeuLysSerG1 737
 Db 1263 CCGAATTCGAGTACAGAGTCC--GTAGAAAACCTGCGAATGTGTATTACCATGA 1319
 QY 737 uGluTyArgArgLysSerLeuLeuMetGluAlaTyTrpLeuArgGlyAsnGlu----- 754
 Db 1320 GCAGCAGCTGCACCTTCAGCATGTGTGCCCACTTACACACAGTATGAGCCTGTGC 1379
 QY 755 -----GluHisIleLysIleIleTrpArgGlnValAs 765
 Db 1380 GGTGATGACATAGGCGAGCTGCAAGTGTGAGGCTCCCAAGTGCATACACAGCTGTGA 1439
 QY 765 PheValAspGluLeuThrArgLysSerTrpLeuValLysGlyMetProLysAspValAl 785
 Db 1440 CAACATCTCCCGAGTCTCT--GTGACAGCATCCACGACGAGAGAGCAAGACCTGT 1496
 QY 785 ThrMetLysLeuArgAspGluLeuArgSerIleSerHisLysMetGluAsnMetAspSe 805
 Db 1497 GTTCATTGACAGAGGAGATCCGCGCGCTTTCGAAACAGCTGCTCATACCCCGAC 1556
 QY 805 r-----ProLeuAspProValTyTrpLysLeuGlyGluMetIleIleAspLys 820
 Db 1557 AGCTTCAAAAGAGACCCAGAAATCT-----TC 1586
 QY 820 AlaIleValLeuGlySerHisAlaTyArgProLeuMetLeuHisTrpLysAsnLys----- 838
 Db 1587 TGCAGTGTCTTC-----AAAGAGCC-----TGACAGAGAAAGTACG 1625
 QY 839 -----AsnProLysSerAspLeuHisLeuPro-----PheCysAl 850
 Db 1626 GCGATCAGAGAGGCTCCCTTACGGC-----CATCTCCCAATGGCGGCTCTGTGC 1679
 QY 850 AsnIlePheLysAsnGlyAspAspLeuArgGlnAspMetLeuValLeuGlnValLeuG1 870
 Db 1680 AGTCATTTCAGTGTGGGATGACCTTCGGCAAGGCTTCTGCGCTTCAAGTGTGAA 1739

QY 805 r-----ProLeuaspProValTyrIysLeuGlyGluMetIleIleAspIy 820
Db 1593 AGCCTTCAACGAGACCCAGAAATCT-----TC 1622
QY 820 sAlaIleValleuGlySerAlaIysArpProLeuMetLeuHisTrpIyAsnIys----- 838
Db 1623 TGCAGTTGCTCTC-----AAAGAGCC-----TGGCAGAGAAAGTACG 1661
QY 839 -----AsnProIysSerAspLeuHisLeuPro-----PheCysAl 850
Db 1662 GCGGATCAGAGAGGCTCCCTACGCGC-----CATCTCCCAATTGGCGGCTCTCTGC 1715
QY 850 aMetIlePheIyAsnGlyAspAspLeuArgGlnAspMetLeuValleuGlnValleuG 870
Db 1716 AGTCATTGTCAGATGTGGGATGACCTTGGCAGAGKCTTCTGGCCTTCAAGTGTGAA 1775
QY 870 uValMetAspAsnIleTrpIyAlaAlaAsnIleAspCysCysLeuAsnProTyrAlaVa 890
Db 1776 GCAACTGCAGTCCATTGGGAACAGGAGCGAGTCCCTTGGATCAAGCCA----- 1827
QY 890 lleuProMetGlyGluMetIleGlyIleIleGluValProAsnCysIysThrIlePh 910
Db 1828 -----ATACAAGATTCTTGT----- 1842
QY 910 eGluIleGlnValGlyThrGlyPheMetAsnThrAlaValArgSerIleAspProSerPh 930
Db 1843 -GAAATTACGACTGATGTGGATGATTAACCAAGTGTCAATGCTGTG----- 1890
QY 930 eMetAsnIyStrpIleArgIysGlnCysGlyIleGluAspGluIyIyAspSerIyIy 950
Db 1891 -----TCCATCCATCAGGTGAAGAAACAGTCAAGCT 1922
QY 950 sAspSerThrIyAsnProIleGluIyIyIleAspAsnThrGlnAlaMetIyIyIyTy 970
Db 1923 CTCCTTGTCTCATTAATCTCTACAGAG-----CAAGCAGTTACCACTGAGGACAT 1976
QY 970 rPheGluSerValAspArgPheLeuIySerCysValGlyTyrSerValAlaThrTyrI 990
Db 1977 CTTCAAGTGCACAGCGCAATTTGTGCAAGTTGTGCTGGTACTGCTGTCTGCTACT 2036
QY 990 eMetGlyIleIyAspArgHisSerAspAsnLeuMetLeuThrGluAspGlyIyTyVa 1010
Db 2037 GCTGCAAGTCAAGACAGACAGACATGGAATATCTTTGAGACGCAAGGCGACATCAT 2096
QY 1010 HisIleAspPheGlyHisIleleuGlyHisIleGlyIyThrIyIleGlnArgAs 1030
Db 2097 CCACATCGACTTGGCTTCACTCTCCAGCTCACCCGAAATCTGGGCTTT-----GA 2150
QY 1030 pArgGlnProPheIleLeuThrGlnHisPheMetThrValIleArgSerGlyIySerVa 1050
Db 2151 GACGTACGCTTTAAGCTTACCAAGATTTGTGATGTGATG-----GGCGGCT 2201
QY 1050 lAspGlyAsnSerHisGluLeuGlnIySpheIyThrLeuCysValGlnAlaTyGluVa 1070
Db 2202 GGATGGCGCATG-----TTCAACTACTATTAAGATGATGCTGCAAGGCGTATGTC 2255
QY 1070 lMetTrpAsnAsnArgAspLeuPheValSerLeuPheThrLeuMet---LeuGlyMetG 1089
Db 2256 CGCTCGAAGAACATGACAGAGTGTGAGATCGTGAATCATCAGCAAGATTTCTCA 2315
QY 1089 uLeuProGluLeuSerThrIyAlaAspLeuAspHisIleuIyIyIyThrLeuPheCysAs 1109
Db 2316 GCTTCTTGTGCTTCAATGCTCCAGCACATTCGAAACCTCAAGAGAGG---TTCACAT 2372
QY 1109 nGlyIySerIyGluGlnAlaArgIySphePheAlaGlyIleTyGluGlnAlaPheAs 1129
Db 2373 GAGCATGACTGAGAGACAGCTGCAGCTG-----CTGTGAGACAGATGTGTGA 2420
QY 1129 nGlySerTrpSerThrIyThrAsnTrpLeuPheHisAlaValIyHis 1145
Db 2421 TGGCAGTATGCGGTATATCACCAAACTTATGACGGCTTCCAGTAC 2469

Search completed: June 6, 2003, 07:57:21
Job time : 989 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 6, 2003, 01:40:09 ; Search time 191 Seconds
(without alignments)
5626.154 Million cell updates/sec

Title: US-08-908-453-2

Perfect score: 3504

Sequence: 1 CGGAAGCCATGAGACTGAG.....ACGACATCAACTACTGA 3504

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued Patents NA: *
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3: /cgn2_6/ptodata/2/ina/6A.COMB.seq: *
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5: /cgn2_6/ptodata/2/ina/PTOS.COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3504	100.0	3504	4	US-08-857-076-47
2	146.4	4.2	3207	1	US-08-162-081B-35
3	146.4	4.2	3207	2	US-08-780-872-35
4	146.4	4.2	3207	4	US-09-085-957-35
5	130	3.7	3240	1	US-08-162-081B-34
6	130	3.7	3240	2	US-08-780-872-34
7	130	3.7	3240	4	US-09-085-957-34
8	130	3.7	3412	1	US-08-162-081B-32
9	130	3.7	3412	2	US-08-780-872-32
10	130	3.7	3412	4	US-09-085-957-32
11	103.6	3.0	5220	3	US-09-357-070-1
12	103.6	3.0	5220	2	US-08-777-405A-1
13	103.6	3.0	5220	2	US-08-977-871A-1
14	103.6	3.0	5220	2	US-09-225-951-1
15	96.4	2.8	3808	2	US-08-916-917-3
16	96.4	2.8	3808	2	US-08-972-631-3
17	96.4	2.8	3808	2	US-08-972-629-3
18	96.4	2.8	3808	2	US-08-972-630-3
19	96.4	2.8	3808	2	US-08-972-630-3
20	96.4	2.8	3808	2	US-08-672-211-3
21	95.6	2.7	3213	3	US-09-225-170-3
22	95.6	2.7	3213	2	US-09-393-350-1
23	90	2.6	5162	3	US-08-916-917-13
24	90	2.6	5162	2	US-09-225-170-13
25	86.8	2.5	4134	2	US-08-817-090B-1
26	86.8	2.5	4137	2	US-08-817-090B-1
27	65.6	1.9	5285	2	US-09-355-160D-1
					US-08-609-049A-29

28	65.6	1.9	5285	4	US-09-170-996-29	Sequence 29, Appl
29	55.4	1.6	7218	1	US-08-232-463-14	Sequence 14, Appl
30	49.8	1.4	6831	2	US-08-609-049A-27	Sequence 27, Appl
31	49.8	1.4	6831	4	US-09-170-996-27	Sequence 27, Appl
32	48.8	1.4	381	1	US-08-162-081B-38	Sequence 38, Appl
33	48.8	1.4	381	2	US-08-780-872-38	Sequence 38, Appl
34	48.8	1.4	381	4	US-09-085-957-38	Sequence 38, Appl
35	48	1.4	393	1	US-08-162-081B-40	Sequence 40, Appl
36	48	1.4	393	2	US-08-780-872-40	Sequence 40, Appl
37	48	1.4	393	2	US-09-085-957-40	Sequence 40, Appl
38	46.8	1.3	3252	4	US-09-118-442-1	Sequence 40, Appl
39	46.8	1.3	3252	4	US-09-677-064-1	Sequence 1, Appl1
40	41.8	1.2	3281	4	US-09-453-702B-85	Sequence 85, Appl1
c	41	1.1	112132	4	US-09-741-150-3	Sequence 3, Appl1
42	36.6	1.0	915	4	US-09-134-001C-1741	Sequence 1741, Ap
43	36.6	1.0	4211	4	US-09-004-838-106	Sequence 106, App
44	35.2	1.0	731	1	US-08-451-405A-2	Sequence 2, Appl1
45	34.8	1.0	1882	4	US-09-370-253-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-08-857-076-47
Sequence 47, Application US/08857076C
Patent No. 6225120
GENERAL INFORMATION:
APPLICANT: Ruvkun, Gary
APPLICANT: Kimura, Koutarou
APPLICANT: Patterson, Garth
APPLICANT: Ogg, Scott
APPLICANT: Paradis, Suzanne
APPLICANT: Tisenbaum, Heidi
APPLICANT: Morris, Jason
APPLICANT: Kowek, Allison
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
FILE REFERENCE: 00786/351001
CURRENT APPLICATION NUMBER: US/08/857,076C
CURRENT FILING DATE: 1997-05-15
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 47
LENGTH: 3504
TYPE: DNA
ORGANISM: Caenorhabditis elegans
US-08-857-076-47

Query Match 100.0%; Score 3504; DB 4; Length 3504;
Best local similarity 100.0%; Pred. No. 0;
Matches 3504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CGGAAGCCATGAGACTGAGATCTGATGCTGACACGAGCGAAGTTCGAGATCTCG	60
DB	1	CGGAAGCCATGAGACTGAGATCTGATGCTGACACGAGCGAAGTTCGAGATCTCG	60
QY	61	CAGATGATGTTAATTTTACATCCACACTGCAAAAGATGTCGAGAGTTCG	120
DB	61	CAGATGATGTTAATTTTACATCCACACTGCAAAAGATGTCGAGAGTTCG	120
QY	121	CGAAGAGCCATGCTGAGACCGAGAAATGCGAAGTTCGCTTCGAAATG	180
DB	121	CGAAGAGCCATGCTGAGACCGAGAAATGCGAAGTTCGCTTCGAAATG	180
QY	181	GGTTCGAGATATCATCATGATGTCATTCGAGAAATTAAGTATGTTTCG	240
DB	181	GGTTCGAGATATCATCATGATGTCATTCGAGAAATTAAGTATGTTTCG	240
QY	241	TGTTTCTTGAATGTCGCAATCGGTGAAATCAAGCTATGATTTCAACATCA	300
DB	241	TGTTTCTTGAATGTCGCAATCGGTGAAATCAAGCTATGATTTCAACATCA	300

QY 301 CTTTGGATTGATGCTCCGATGAGTGGGGAACATATTCGTTAAGCCACAGATTAT 360
 Db |||||
 Db 301 CTTTGGATTGATGCTCCGATGAGTGGGGAACATATTCGTTAAGCCACAGATTAT 360
 QY 361 GTGTTCAGACAGTTGAATTAATTCGCGCAAAATGGAATTATTTAAGCAGCATCAACC 420
 Db |||||
 Db 361 GTGTTCAGACAGTTGAATTAATTCGCGCAAAATGGAATTATTTAAGCAGCATCAACC 420
 QY 421 CTGTGAAATTAGAGCTCAGCGGCACTTCCCAATGCTTTTCTCTACCAACTGATGA 480
 Db |||||
 Db 421 CTGTGAAATTAGAGCTCAGCGGCACTTCCCAATGCTTTTCTCTACCAACTGATGA 480
 QY 481 ATAAAACAGGATTAAGAAATTAATGATGATATAGTCAATGCTGATGATCACTGAT 540
 Db |||||
 Db 481 ATAAAACAGGATTAAGAAATTAATGATGATATAGTCAATGCTGATGATCACTGAT 540
 QY 541 AAACCTGGAAGAGCCTCGATAGAGAACTCCGTCATATTCGCTTCTCTGCGCTCGT 600
 Db |||||
 Db 541 AAACCTGGAAGAGCCTCGATAGAGAACTCCGTCATATTCGCTTCTCTGCGCTCGT 600
 QY 601 ACGAAGAAAACGCTGCTTGAACAGTGAATTGGAGGGAACAGTCACTACGCTTCCCGAA 660
 Db |||||
 Db 601 ACGAAGAAAACGCTGCTTGAACAGTGAATTGGAGGGAACAGTCACTACGCTTCCCGAA 660
 QY 661 GAACGATCTGTGTGTGTGATGATGTCGCCGAAAGATTTGGAATCAAAAGTCAAGCT 720
 Db |||||
 Db 661 GAACGATCTGTGTGTGTGATGATGTCGCCGAAAGATTTGGAATCAAAAGTCAAGCT 720
 QY 721 GCCAAGCTGATTCAGATGTTTTGAGAAAAACGTTAAACGGAATCAATGAGATTGCT 780
 Db |||||
 Db 721 GCCAAGCTGATTCAGATGTTTTGAGAAAAACGTTAAACGGAATCAATGAGATTGCT 780
 QY 781 GAGAAAATGATGAATTCAAATTTGAATTCAGATCCGAAAGAAATCCGAAATCTCTGCT 840
 Db |||||
 Db 781 GAGAAAATGATGAATTCAAATTTGAATTCAGATCCGAAAGAAATCTCTGCT 840
 QY 841 CACAGCTTCTCTACGAAATGCGAAAAATGATGATGATACGATACCGATATCTGCAAT 900
 Db |||||
 Db 841 CACAGCTTCTCTACGAAATGCGAAAAATGATGATGATACGATACCGATATCTGCAAT 900
 QY 901 GAAGATGCTTCTCTCAATTTGCTGACGCTACACGTTTGTTCAAATCAGATGTCAA 960
 Db |||||
 Db 901 GAAGATGCTTCTCTCAATTTGCTGACGCTACACGTTTGTTCAAATCAGATGTCAA 960
 QY 961 CTTAGCTCTTAATGATGCTCCGTTGCGAACTGGAAGATGATGATGCTGCTGATTCCT 1020
 Db |||||
 Db 961 CTTAGCTCTTAATGATGCTCCGTTGCGAACTGGAAGATGATGATGCTGCTGATTCCT 1020
 QY 1021 GTTCCGCGCAATCACTAGTCTCTCAAAAGACTATTTGTCGCCCAAAACCACTACGAA 1080
 Db |||||
 Db 1021 GTTCCGCGCAATCACTAGTCTCTCAAAAGACTATTTGTCGCCCAAAACCACTACGAA 1080
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 Db |||||
 Db 1081 CATTAATGAGAGCACAGAAAGAAATCTTGCTCTAGACGTGCTCAGCGTCTATAGAT 1140
 QY 1141 ACCACACCAAAACAGAGCAAGAACAGTGCATGCTTATGATGATGATTTGTCGCAAGCT 1200
 Db |||||
 Db 1141 ACCACACCAAAACAGAGCAAGAACAGTGCATGCTTATGATGATGATTTGTCGCAAGCT 1200
 QY 1201 TCACTCAAAAGATTCACTTTGCGACCTTGAACGCAATCTTATGATGATGATTTGAT 1260
 Db |||||
 Db 1201 TCACTCAAAAGATTCACTTTGCGACCTTGAACGCAATCTTATGATGATGATTTGAT 1260
 QY 1261 ATTTCTGATGATGATTTCCCGCGCAGCTGATGATGATGATGATGATGATGATGAT 1320
 Db |||||
 Db 1261 ATTTCTGATGATGATTTCCCGCGCAGCTGATGATGATGATGATGATGATGATGAT 1320
 QY 1321 TATGTGGGAGCACTGACGCTGGGATCAAAATCTACAAAGAAAGTGAATGCTCAATTTGA 1380
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 QY 1381 AATGGAATTAAGAAATGTAACCTTTGATCTATACATGAGAGATGACCATCTGCA 1440

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 Db |||||
 Db 1441 GTACTCAGACTTCGCTGTTTGTACCGAAAGTGAATTTAAAGTGAAGATTGGAATT 1500
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 Db 1501 GGTGTGGGAATTAATGATGCTTACCGAATTTGAGAGATGATGATGATGATGATGATGAT 1560
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 Db |||||
 Db 1561 TTCCATCTGTGGGCTCTCGAAGCCGACCTGCAATGATGATGATGATGATGATGATGAT 1620
 QY 1621 AGATAGGACCAACGACCGCTTACAAATTTCAATGATTTGATGATGATGATGATGATGAT 1680
 Db |||||
 Db 1621 AGATAGGACCAACGACCGCTTACAAATTTCAATGATTTGATGATGATGATGATGATGAT 1680
 QY 1681 ATGCCAGTCAAGAGCAATACATATCTGTCAGAGCCGAGATCTTGACCGAACT 1740
 Db |||||
 Db 1681 ATGCCAGTCAAGAGCAATACATATCTGTCAGAGCCGAGATCTTGACCGAACT 1740
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 Db |||||
 Db 1741 TTGAATATTATGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
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 QY 1861 GTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
 Db |||||
 Db 1861 GTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
 QY 1921 GAACCTGCTATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
 Db |||||
 Db 1921 GAACCTGCTATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
 QY 1981 AAATGGAACCGCGAGTGTGACGACCGCTGTCATTTGCTGGAAGAACTTGCACGAT 2040
 Db |||||
 Db 1981 AAATGGAACCGCGAGTGTGACGACCGCTGTCATTTGCTGGAAGAACTTGCACGAT 2040
 QY 2041 CGTGTGATTCGAAAGTTTGAAGTGAAGTGAATGATGATGATGATGATGATGATGATGAT 2100
 Db |||||
 Db 2041 CGTGTGATTCGAAAGTTTGAAGTGAAGTGAATGATGATGATGATGATGATGATGATGAT 2100
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 Db |||||
 Db 2101 CATCTTTTCATATGCTCTCTATACAGGCGTTGAAGTACGAACCGCGTCAATCGAA 2160
 QY 2161 GTTGAATGATGCTCTTACATGAGCTCTGCGCATTTACGAATTTGATGATGATGATGAT 2220
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 Db 2161 GTTGAATGATGCTCTTACATGAGCTCTGCGCATTTACGAATTTGATGATGATGATGAT 2220
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 Db 2221 TGGCTGCTCCGTCAGAGATTTGCTGTTGAGAGTTGATGATGATGATGATGATGATGAT 2280
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 Db 2281 CGCCGCTATCTCACTTCTGATGGAAGCTTACCTCGCTGGAATGAGAGACATCAAGATC 2340
 QY 2341 ATCACCAGCAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2400
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 Db 2341 ATCACCAGCAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2400
 QY 2401 ATGCCAAAGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460
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 QY 2461 ATGCAAAAGATGTTGCTACAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 2520

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Db	2521	AAAGCATTCGTCTCTAGGAAGTGCAGAAAGTCCGTAAATAGCTTCACTCGAAGACAAAT	2580
Qy	2581	CCAAAGATGACCTGCACCTTCGGTTCGTGCAATGATCTTCAGAAATGAGAGCATCTT	2640
Db	2581	CCAAAGATGACCTGCACCTTCGGTTCGTGCAATGATCTTCAGAAATGAGAGCATCTT	2640
Qy	2641	CGCCAGACATGCTTGTTCCTCAAGTTCGAAATTATGATTAACATCTGGAAGCTGCA	2700
Db	2641	CGCCAGACATGCTTGTTCCTCAAGTTCGAAATTATGATTAACATCTGGAAGCTGCA	2700
Qy	2701	AAACATTTGATCTGTGTTGAACCCCGTACGCAAGTCTTCCAAATGGAGAAATATGGAATT	2760
Db	2701	AAACATTTGATCTGTGTTGAACCCCGTACGCAAGTCTTCCAAATGGAGAAATATGGAATT	2760
Qy	2761	ATTGAAGTGTGCTTAATTTGTAAAAACAATATTCCGAGTTCAAGTTGGAACAGATTCA	2820
Db	2761	ATTGAAGTGTGCTTAATTTGTAAAAACAATATTCCGAGTTCAAGTTGGAACAGATTCA	2820
Qy	2821	AATACAGAGTTCCGAGTATTGATCTTCGTTTATGAAATAAGTGATTCGAAACAATGC	2880
Db	2821	AATACAGAGTTCCGAGTATTGATCTTCGTTTATGAAATAAGTGATTCGAAACAATGC	2880
Qy	2881	GGAATTGGAATGGAAGAAAGAAAGAAAGCAAAAGCACTACGAAAGAAACCCATGGAAAG	2940
Db	2881	GGAATTGGAATGGAAGAAAGAAAGAAAGCAAAAGCACTACGAAAGAAACCCATGGAAAG	2940
Qy	2941	AAGATTGATAATTAATCTCAAGCCATGAGAAATATTTTGAAGTGTGATCGATTCCCTATAC	3000
Db	2941	AAGATTGATAATTAATCTCAAGCCATGAGAAATATTTTGAAGTGTGATCGATTCCCTATAC	3000
Qy	3001	TCGCTGTGTGGAATATTCAATTGTCACGTAATATGGAATTCAGATTCGTAACGAT	3060
Db	3001	TCGCTGTGTGGAATATTCAATTGTCACGTAATATGGAATTCAGATTCGTAACGAT	3060
Qy	3061	AATCTGATGCTCACTGAGAGTGAAGAAATATGTCACATTTGATTCGCTCAATTTGGGA	3120
Db	3061	AATCTGATGCTCACTGAGAGTGAAGAAATATGTCACATTTGATTCGCTCAATTTGGGA	3120
Qy	3121	CACGGAAGACCAAACTTGGGATCCAGGAGATCGTCAACCGTTATTCTAACCGAACAC	3180
Db	3121	CACGGAAGACCAAACTTGGGATCCAGGAGATCGTCAACCGTTATTCTAACCGAACAC	3180
Qy	3181	TTTATGACAGTATTCGATTCGGGTAAATCTGTGATGGAATTTGGCATGACTACAAAA	3240
Db	3181	TTTATGACAGTATTCGATTCGGGTAAATCTGTGATGGAATTTGGCATGACTACAAAA	3240
Qy	3241	TTTCAAAAAGTATGCTGGAAGCCTTCAAGATTAATGTCGATTAATCGAATTTTGTGCTT	3300
Db	3241	TTTCAAAAAGTATGCTGGAAGCCTTCAAGATTAATGTCGATTAATCGAATTTTGTGCTT	3300
Qy	3301	TCCTTGTTCACCTTGATGCTCGGAATGGAATTGCTGAGCTGTGCGAAGAAAGCGAATTTG	3360
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Qy	3361	GATCATTTGAAGAAACCCCTCTTCTGCAATGAGAAACAAAGAAAGCAAGAAAGTTT	3420
Db	3361	GATCATTTGAAGAAACCCCTCTTCTGCAATGAGAAACAAAGAAAGCAAGAAAGTTT	3420
Qy	3421	TTGCTGTGAATCTACGAAGAAAGCCTTCAATGATCATGTGTCTACAAACGAATTTGGCTC	3480
Db	3421	TTGCTGTGAATCTACGAAGAAAGCCTTCAATGATCATGTGTCTACAAACGAATTTGGCTC	3480
Qy	3481	TTTCAACGAGTCAAACACTACTGCA 3504	
Db	3481	TTTCAACGAGTCAAACACTACTGCA 3504	

RESULT 2
US-08-162-081B-35

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? Sequence 35 Application US/08162081B
? Patent No.5824492
?
? GENERAL INFORMATION:
? APPLICANT: Hilee, Ian Donald; Fry, Michael John; Dhand, Ritu
? APPLICANT: Balai, Waterfield, Michael Derek; Parker, Peter
? APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
? APPLICANT: Stefano; Gout, Ivan Tarasovitch
? TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
? TITLE OF INVENTION: THEIR PREPARATION AND USE
? NUMBER OF SEQUENCES: 50
?
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Felfe & Lynch
? STREET: 805 Third Avenue
? CITY: New York
? STATE: New York
? COUNTRY: USA
? ZIP: 10022
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
?
? COMPUTER: IBM PS/2
? OPERATING SYSTEM: PC-DOS
? SOFTWARE: Wordperfect
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/162,081B
? FILING DATE: February 7, 1994
?
? CLASSIFICATION: 435
?
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: PCT/GB93/00761
? FILING DATE: 13 April 1993
? ATTORNEY/AGENT INFORMATION:
? NAME: Pasqualini, Patricia A.
? REGISTRATION NUMBER: 34,894
? REFERENCE/DOCKET NUMBER: LUD 5256
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (212) 688-9200
? TELEFAX: (212) 838-3884
? INFORMATION FOR SEQ ID NO: 35:
?
? SEQUENCE CHARACTERISTICS:
? LENGTH: 3207 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
?
? US-08-162-081B-35

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Db 1828 ATGGTTCGAGGTTTGTCTGTCGTCCTAGAAAAATATTTAAACAGATGACAAACTTCT 1887
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 QY 2164 GGAATGATGCTCTTGACTAGAGCTCTGCGATTAATGCAATTTGACATCGACTTTTCG 2223
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 Db 2068 TCTATTTCCGTCGATGAGGATGTATCTGAAGCACTTTAATGAGCAAGTTGAGCTATG 2127
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 Db 2188 GTACAGATGAAGTTTATGTTGA---GCAAAATGCGCGACACAGATTCATGATGCTCTC 2244
 QY 2464 GAAATATGATTCCTCCACTGGAATCTGTGTACAACTGCGGGAATGATATATGACAAA 2523
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 QY 2644 CAGGACATGCTTGTCTCAAGTCTCGAAGTATGAGTAACATCTGAAAGCTCCAAAC 2703
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 QY 2884 ATTGAAGTGAAGAAAGAAAGCAAAAGAGCTCTAGAAAAATCCATCGAAAAGAG 2943
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 QY 2944 ATTGATTAATCTCAAGCATGAGAAATTTTGAAGTGTGATGATTCCTATATCTCG 3003
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 Db 2701 TGTGCTGATATATGTTGTCACCTTCAATTTGGAAATTTGAGATGTCACAAATGATAT 2760
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QY 3184 ATGACAGTATTCATCGGCTAAATCTGTGATGGAATTCGCATGAGCTACAAAAATTC 3243
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 QY 3244 AAAAGTTATCGTTCGAGAGCCCTACAGAAATTAATGGAATTAATGAGATTTTCTTTC 3303
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 QY 3424 GCTGGAATCTACGAGAAAGCCCTCAATGATCATGCTTACCAAAACGATTTGCTTTC 3483
 Db 3118 ATGAAACAAATGAATGATGACACCATGTGTGGCTGGAACAAAAATGATTTGATCTTC 3177
 QY 3484 CACGCACTCAACA 3497
 Db 3178 CACCAATTAAGCA 3191

RESULT 4
 US-09-085-957-35
 ; Sequence 35, Application US/09085957
 ; Patent No. 6274327
 ; GENERAL INFORMATION:
 ; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
 ; APPLICANT: Bale, Waterfield, Michael Derek; Parker, Peter
 ; APPLICANT: Joseph, Obeu, Masayuki; Panayotou, George; Volinia,
 ; APPLICANT: Stefano; Gout, Ivan Tarasovich
 ; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
 ; TITLE OF INVENTION: THEIR PREPARATION AND USE
 ; NUMBER OF SEQUENCES: 50
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Felfe & Lynch
 ; STREET: 805 Third Avenue
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10022
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: Wordperfect
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/085, 957
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/780, 872
 ; FILING DATE: 09-JAN-1997
 ; APPLICATION NUMBER: 08/162, 081
 ; FILING DATE: February 7, 1994
 ; APPLICATION NUMBER: PCT/GB93/00761
 ; FILING DATE: 13 April 1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Pasqualini, Patricia A.
 ; REGISTRATION NUMBER: 34,894
 ; REFERENCE/DOCKET NUMBER: LUD 5256
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 688-9200
 ; TELEFAX: (212) 838-3884
 ; INFORMATION FOR SEQ ID NO: 35:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3207 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single

TOPOLOGY: linear
US-09-085-957-35

Query Match 4.2%; Score 146.4; DB 4; Length 3207;
Best Local Similarity: 45.9%; Pred. No. 4.6e-35;
Matches 723; Conservative 0; Mismatches 761; Indels 90; Gaps 3;

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DB 1708 CTGTCTGTTAAATGAACTCTAGAGATGAAAGTACTGATGATGCTGCTGTTAAAAAGT 1767
QY 1984 TGGAAACCGCCGAGTGTGGCAGCCGCTTGACTTTGCTTGAAAAAGTTCACGAGTCT 2043
DB 1768 TGGCCTCCAAATGAACTGAAAGGCTATGAGCTTTGCTGATGCAATTAACCAATCTCT 1827
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DB 1828 ATGTTTCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1887
QY 2104 CTTTCATATTCCTCTCATACAGGCTTGAAGTACGAAACCGCTGCTCAATCGGAAGT 2163
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QY 2164 GGAATGATGCTCTGCTGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2223
DB 1948 GTGAGATTTTACTCAAAAAAGCCTTAATCAAGATGAGTCTGCTGCTGCTGCTGCTGCT 2007
QY 2224 CTGCTCCGTCGAGAGATTGCTGTTGAGAGATTGATCTGAATTAAGTGAAGATATGCG 2283
DB 2008 CATTTAAATCTGAGATGAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2067
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DB 2068 TCCATTCGCTGCTGATGAGTGAATGATCTGAAGCAGCTTAATGAGAGATGAGCTATG 2127
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DB 2305 TGTGCAATTAATGCTCTGCAAAAGGCACTGTGTTGAATGGAGAAACCAAGATC 2364
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DB 2485 CTTGATCTTGAATGATGATCTTAATGATGATGATGATGATGATGATGATGATGATGAT 2544
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QY 2824 ACAGAGTTCGAGATGATGATCTTCTGTTATGAATTAATGAGATTCGGAACATGCGGA 2883
DB 2598 ----- 2597
QY 2884 ATTGAAGATGAAAGAAAGCAAAAGAGCTTACGAAATTAATCCATCGAAAGAG 2943

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DB 2598 -----GAAAGTGCACCTGAGTTTAAACAGCACACACATCCATCAATG 2640
QY 2944 ATTGATTAATCTCAACCATTAAGAAATATTTGAAATGTCGATTCCTATCTACG 3003
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DB 3178 CACACATTAAGCA 3191

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RESULT 5
US-08-162-081B-34
; Sequence 34, Application US/08162081B
; Patent No. 582492
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Balas, Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph, Otsu, Masayuki; Panayotou, George; Volinda,
; APPLICANT: Stefano; Gout, Ivan Teresovitch
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESS: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08162,081B
; FILING DATE: February 7, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00761

FILING DATE: 13 April 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Pasqualini, Patricia A.
 REGISTRATION NUMBER: 34,894
 REFERENCE/DOCKET NUMBER: LUD 5256
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 688-9200
 TELEFAX: (212) 838-3884
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3240 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-162-081B-34

Query Match 3.7%; Score 130; DB 1; Length 3240;
 Best Local Similarity 45.7%; Pred. No. 6,2e-30;
 Matches 719; Conservative 0; Mismatches 765; Indels 90; Gaps 4;

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 1708 CTGCTGTTAATGAAATTTCTAGATGAGTAGCCGATGATATGCTTGTAAAGAT 1767
 1984 TGGAAACCGCGAGTGTGGACCGCGTTGACTTTGTTGAAAAGTTGACGATCGT 2043
 1768 TGGCTCCCAATCAACCTGAAACAGGCTATGAACTTGTGA CTGTAATTAACCAATCT 1827
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 1888 CAGTATTTAATCTACCTAGTACAGGCTCTAAATATGAAACAATTTGGATACTTGGT 1947
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RESULT 6

US-08-780-872-34

Sequence 34, Application US/08780872

Patent No. 5846824

GENERAL INFORMATION:

APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu

APPLICANT: Balaj, Waterfield, Michael Derek; Parker, Peter

APPLICANT: Joseph, Otsu, Masayuki; Panayotou, George; Volinia,

APPLICANT: Stefano, Gout, Ivan Tarabovitch

TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESS: Felife & Lynch

STREET: 805 Third Avenue

CITY: New York

STATE: New York

COUNTRY: USA
 ZIP: 10022
 COMPUTER READABLE FORM:
 MEDID TYPE: Diskette, 5.25 inch, 360 kb storage
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: Wordperfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/06/780,872
 FILING DATE: 09-JAN-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/162,081
 FILING DATE: February 7, 1994
 APPLICATION NUMBER: PCT/GB93/00761
 FILING DATE: 13 April 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Pasqualini, Patricia A.
 REGISTRATION NUMBER: 34,894
 REFERENCE/DOCKET NUMBER: LUD 5256
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 688-9200
 TELEFAX: (212) 838-3884
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3240 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-780-872-34

Query Match 3.7%; Score 130; DB 2; Length 3240;
 Best Local Similarity 45.7%; Pred. No. 6,2e-30;
 Matches 719; Conservative 0; Mismatches 765; Indels 90; Gaps 4;

QY 1924 CTCGATTTGTGTGACGTGAGAACTTTCCGACCTCATGTGATGCTTGAANA 1983
 DB 1708 CTGTCTGTTAAATGGAATCTAGAGATGAAGTAGCCAGATGATTTGCTGAANAAGAT 1767
 QY 1984 TGGAAACGCCGAGTGTGGCAGCCGCTTGACTTTGCTTGAANAAGATGCGATGCT 2043
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RESULT 7
 US-09-085-957-34

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Sequence 34, Application US/09085957
Patent No. 6274327
GENERAL INFORMATION:
APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter
APPLICANT: Joseph, Oden, Masayuki; Panayotou, George; Volinia,
APPLICANT: Stefano, Gout, Ivan Tarasovitch
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felte & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,957
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/780,872
FILING DATE: 09-JAN-1997
APPLICATION NUMBER: 08/162,081
FILING DATE: February 7, 1994
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5256
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 3240 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-085-957-34
Query Match 3.7%; Score 130; DB 4; Length 3240;
Best Local Similarity 45.7%; Pred. No. 6.2e-30;
Matches 719; Conservative 0; Mismatches 765; Indels 90; Gaps 4;
QY 1244 CTCGCAATTTGTTGACCTGATCGTGAAGAACTTTTCGAGCTCTATGTGATGCTTGAAGAA 1983
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DB 2641 CTCAAAGCAAGAACAAAGAAATATATGATGACGACATTCGCTTTACAGCTTCA 2700
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RESULT 8
US-08-162-081B-32
Sequence 32, Application US/08162081B
Patent No. 5824492
GENERAL INFORMATION:
APPLICANT: Hiles, Ian Donald, Fry, Michael John, Dhand, Ritu
APPLICANT: Bala, Walefield, Michael Derek, Parker, Peter
APPLICANT: Joseph, Otsu, Masayuki, Panayotou, George, Volinia,
APPLICANT: Stefano, Gout, Ivan Tarasovitch
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
TITLE OF INVENTION: THEIR PREPARATION AND USE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,081B
FILING DATE: February 7, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5256
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 3412 base pairs
TYPE: nucleic acid
STRANDEDNESS: single or double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3204
OTHER INFORMATION: /standard_name= "CDS"
US-08-162-081B-32
Query Match 3.7%; Score 130; DB 1; Length 3412;
Best Local Similarity 45.7%; Pred. No. 6.4e-30;
Matches 719; Conservative 0; Mismatches 765; Indels 90; Gaps 4;
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RESULT 9 US-08-780-872-32

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; Sequence 32, Application US/08780872
; Patent No. 5846824
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
; APPLICANT: Stefano; Gout, Ivan Tarasovich
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,872
; FILING DATE: 09-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/162,081
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: PCT/GB93/00761
; FILING DATE: 13 April 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: LUD 5256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3684
; INFORMATION FOR SEQ ID NO: 32:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 3412 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single or double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3204
; OTHER INFORMATION: /standard_name="CDS"
; US-08-780-872-32

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Query Match      3.7%; Score 130; DB 2; Length 3412;
Best Local Similarity 45.7%; Pred. No. 6.4e-30;
Matches 719; Conservative 0; Mismatches 765; Indels 90; Gaps 4;

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Qy      2044 GTGATTCGAAGATTGACAGTGAAGATGTAATGACAGCTGAGCCGCTCAATTCAT 2103
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Qy 3064 CTGATGCTCACTGAGATGAAATAATGTCACATTTTGGGTGATTCGATTCGAGAC 3123
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Qy 3124 GGAAGACCAAACTTGGATTCAGCGAGATCGTCAACCGTTTATTTCAACGAAACCTT 3183
Db 2821 AAGAAAGAAAAATTTGCTTATTAAGAGAAACGTGTCCATTTGTTTGAACAGATTTTC 2880
Qy 3184 ATGACATGATTCGATCGGTAAATCTGTGATGGAATTCGATGAGCTACAAAATTC 3243
Db 2881 TTAAATAGTATTAAGAAAGAGCCCAAGAAATGCACAAGAAATTTGAGAGTTT 2940
Qy 3244 AAAAGCTTATGCGTGAAGCCTACGAAGTATGTGAAATATCGATTTGTTGTTCC 3303
Db 2941 CAGGAGATGTTCACAGCTTATCTAGCTATTTGACAGATGCCATCTTTCATTAAT 3000
Qy 3304 TTGTTACCTTATGCTCGAAATGAGTTGCTGAGCTGTGCAAGAAACGATTTGAT 3363
Db 3001 CTTTCTCATATGATGCTGCTCGAATGCGAAGCTCAATCTTTGATGACATGCA 3060
Qy 3364 CATTTGAGAAAACTCTTCTTGCAATGAGAAAGAAAGAGCGGAAAGTTTTC 3423
Db 3061 TACATTCGAAAGACCTTACCTTAGATA--AACTGACAGAAAGCTTTGAGTATTTTC 3117
Qy 3424 GCTGATCTACGAGAGAGCTTCAATGATCATGCTTACCAAAACGATGGCTCTTC 3483
Db 3118 ATGAAACAATGATATGATCATCATCTGCTGAGCAACAATAATGATTCCTTC 3177
Qy 3484 CAGCAGTCAACA 3497
Db 3178 CACACATTAACA 3191

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OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,957
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/780,872
FILING DATE: 09-JAN-1997
APPLICATION NUMBER: 08/162,081
FILING DATE: February 7, 1994
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5256
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 3412 base pairs
TYPE: nucleic acid
STRANDEDNESS: single or double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3204
OTHER INFORMATION: /standard_name="CDS"
US-09-085-957-32

Query Match 3.7%; Score 130; DB 4; Length 3412;
Best Local Similarity 45.7%; Pred. No. 6.4e-30;
Matches 719; Conservative 0; Mismatches 765; Indels 90; Gaps 4;

Qy 1924 CTCGATTTGTTGAGTCTGATCGTGAAGAACTTTCCGAGCTCTATGATGCTTGAAGAA 1983
Db 1708 CTGCTGTTAAATGAAATTTCTAGAGATGAAGTACCCAGATGTAATGCTTGAAGAAAT 1767
Qy 1984 TGGAAACCCGAGTGTGGACAGCCGCTTGAATTTGCTTGAAGAAAGCTTGAACGAGATCT 2043
Db 1768 TGGCTCCAAATCAACCTGGAACAGGCTATGGAATCTTGACTGTAAATTAACCGAGATCT 1827
Qy 2044 GTGATTCGAAGCTTGGACGTGAGAAAGTGAATGAGCAGCTGAGCCGCTGACATTCAT 2103
Db 1828 ATGTTGAGAGTTTGTCTGCTGCTGCTTGAAGAAATATTTTAACATGACAACTTTCT 1887
Qy 2104 CTTTCATATTCCTCTCATACAGGCGTTGAAGTGAACCGGCTCAATCGGAAGTT 2163
Db 1888 CAGTATTTAATTCAGCTAGTACAGTCTCTTAATAATGAACAATATTTGGATTAACCTGCTT 1947
Qy 2164 GGAATGATGCTTTGACTAGAGCTCTCTGCAATTAATGCAATTTGACATGACATTTCTGG 2223
Db 1948 GTGAGATTTTAACTGAAGAAAGCAATGACTAATCAAGATTTGGGCACTTTTCTTTTGG 2007
Qy 2224 CTGCTCCGTCGAGAGATGCTCTGTTGAGAGATGATGATGGAAGAAAGTGAATATGCG 2283
Db 2008 CATTTAAATCTGAATGACACATTAACAGTTAGCCAGAGTTTGGCTGCTTTGGAG 2067
Qy 2284 CGTATCTCACTCTGATGGAAGCTTACCTCGGTGAATGAAGAGACATCAAGATCATC 2343
Db 2068 TCTTATTTGTCGATGATGAGATGATTAATTTGAAGCACTGAAATGAGCAAGTGAAGCATG 2127
Qy 2344 ACCGCAAGTTGACATGATGATGATGCTCAACAGATGACATCTTGTCAAGGAATG 2403
Db 2128 GAAAGCTCATTAATTAATGACATCTCAACAGAGAGAGAGAGAGAAACACAAAG 2187
Qy 2404 CCAAAAGATGTTGCTACAGATGAAGTGGGTGACGAGCTTGAATGATTAATGATTAATG 2463
Db 2188 GTAC-AGATGAAGTTTATGTTGAGCAAAATGAGGAGCAAGAT--TTATGATGATCCCTTA 2244
Qy 2464 GAAATATGATTTCTCACTGATCTCTGTATCAAACTGGGTGAATGATATATGACAAA 2523

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RESULT 10
US-09-085-957-32
Sequence 32, Application US/09085957
Patent No. 6274327
GENERAL INFORMATION:
APPLICANT: Hiles, Ian Donald, Fry, Michael John, Dhand, Ritu
APPLICANT: Bala, Waterfield, Michael Derek, Parker, Peter
APPLICANT: Joseph, Oseu, Masayuki, Panayotou, George, Volinia,
APPLICANT: Stefano, Gout, Ivan Tarasovitch
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felle & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2

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Db      2245 CAGGGCTGCTGCTCTCTTAACCTGCTCACTCACTGAAGAACTCAGGCTTAAAG 2304
Qy      2524 GCCATGCTCTAGAGAGCAAGCCGCTTAAGCTTCACTGAGAAACAAATCA 2583
Db      2305 TGTCCAAATTATGCTCTTGGCAAAAGGCACTGTGTGTAATTTGGAGAACCAAGCATC 2364
Qy      2584 AAGAGTGAACCTGACCTTCCGTTCTGTGCAATGATCTTCAAGATGAGACGATCTTGC 2643
Db      2365 ATGTAGAGTTACTGTGTTGAGAACATGATCATCTTTAAATGGGATGATTTACGG 2424
Qy      2644 CAGGACATGCTTGTCTTCAAGTTCTCGAAGTTATGATTAACATCTGAAAGCTGCAAC 2703
Db      2425 CAAGATATGCTAACTTCAAAATTTTCTATTAAGAAATATCTGGCAAAATCAAGGT 2484
Qy      2704 ATTTATGCTGTTTGAACCCGTAACGAGTTCTTCCAAATGGAGAAATGTTGAATTTAT 2763
Db      2485 CTTGATCTTGCATGTATCTTATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2544
Qy      2764 GAAGTTGTGCTTAATTTGTAACAATATTCAGATTCAGATTCAGATTCAGATTCAGAT 2823
Db      2545 GAGGTGTGTGCAAAATTTCTCACTATTTATGCAAAATTCAGTGCAGAAAGCGGCTT----- 2597
Qy      2824 ACAGCAGTTGCGAGTATGATCTTCTGTTATGAATTAAGTGAATTCGAAACATGCGGA 2883
Db      2598 ----- 2597
Qy      2884 ATTGAAGATGAAGAAAGAAAGCAAAAGACTCTAGCAAAATTCCTCGAAAGAG 2943
Db      2598 -----GAAAGTGCACTGCAAGTTTCACAGCCACACACTACATCATGCG 2640
Qy      2944 ATTTGATTAATCTCAAGCCATGAAGAAATTTTGAAGTGTGATGATGATGATGATGATG 3003
Db      2641 CTCAAGACAAACAAAGAGAAATATATATGATGATGATGATGATGATGATGATGATGATG 2700
Qy      3004 TGTGTTGATTTCAAGTTCACGATCATATATGAGATTCAGATTCAGATTCAGATTCAG 3063
Db      2701 TGTGTTGATTTCAAGTTCACGATCATATATGAGATTCAGATTCAGATTCAGATTCAG 2760
Qy      3064 CTGATGCTCACTGAAGATGAGAAATATATGATGATGATGATGATGATGATGATGATGATG 3123
Db      2761 ATCATGAGAAAGAGATGAGAACTGTTTCAATATGATTTTGAACATTTTGTGATC 2820
Qy      3124 GAAAGACCAAACTTGGATTCAGGAGATGCTCAACGTTTATTTCAACGACACTT 3183
Db      2821 AAGAGAAATTTTGTATTAACGAGACGTGTGCAATTTTGTGACAGATTTT 2880
Qy      3184 ATGACAGTATTCGATCGGTAATCTGTGATGAGAAATTCGATGATGATGATGATGATG 3243
Db      2881 TTAATATGATTAAGAAAGAGCCCAAGATGCAAAAGCAAGAAATTTGAGGTTT 2940
Qy      3244 AAAAGCTTATGCTGAGAGCTTCAAGATGATGATGATGATGATGATGATGATGATGATG 3303
Db      2941 CAGGAGATGTGTTAAGAGCTTATCTAGCTATTCAGACGATGCCAATCTCTTCATTAAT 3000
Qy      3304 TTGTTACCTTGATGCTGGAATGAGATGCTGAGCTGTGACGAAAGCGGATTTGAT 3363
Db      3001 CTTTCTCAATATGATGCTGCTGCTGATGATGCAAACTTCAATCTTTGATGATGATGATG 3060
Qy      3364 CATTTGAAGAAACCTCTTCTGCAATGAGAAAGCAAGAGAGAGAGAGAGAGAGAGAGAG 3423
Db      3061 TACATTTCAAGAGACCTTACCTTAGTA--AACTGAGCAAGAGAGAGAGAGAGAGAGAG 3117
Qy      3424 GCTGGAATCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3483
Db      3118 ATGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3177
Qy      3484 CACGAGTCAAGCA 3497
Db      3178 CACACATTAACA 3191

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RESULT 11

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US-09-357-070-1
; Sequence 1, Application us/09357070
; Patent No. 5046049
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowart
; TITLE OF INVENTION: ANTISENSE MODULATION OF P13 KINASE P110 DELTA EXPRESSION
; FILE REFERENCE: RTS-0076
; CURRENT APPLICATION NUMBER: US/09/357,070
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 3868
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (197)..(3311)
US-09-357-070-1

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Query Match      3.0%; Score 103.6; DB 3; Length 3868;
Best Local Similarity 53.7%; Pred. No. 1.2e-21;
Matches 264; Conservative 0; Mismatches 219; Indels 9; Gaps 2;

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Qy      3000 CTCGTTGTTGATATTCAGTTGCCAGTACATATATGGAATCAAGATTCGACAGTGA 3059
Db      2827 CTCCTGTGCTGCTATTTGTGTGCGCAATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2886
Qy      3060 TAATGTATGCTCACTGAAGATGAGAAATATGTCATATGATTTGCTGATATTTGGG 3119
Db      2887 CAACATCATGATCCAGAGAGAGTGGGCACTGTTCCATTTGATTTTGGCACTTTCTGGG 2946
Qy      3120 ACAGGAAAGCAAACTTGGATTCAGAGAGATGATGATGATGATGATGATGATGATGATGATG 3179
Db      2947 GAATTTCAAGCAAGTTGGAATTCACCGAGAGTGTCCATTCATCTTCACTACGA 3006
Qy      3180 CTTTATGACAGTATTCGATCGGTAATCTGTGATGGAATTCGATGATGATGATGATGATGATG 3239
Db      3007 CTTTGTCCATGATGATTCAGCAGGGGA-----GACTAATATATGATGAAATTTGAAAG 3060
Qy      3240 ATTCAAAAGTTATGCTGAGAGCTTACGAAGTAATGGAATTAATGAGATTTGTCGT 3299
Db      3061 GTTCGGGGCTACATGTAAGAGGGCTTACACCATCTGTGGGGCCACGGGCTTCTTCTCT 3120
Qy      3300 TTCTTGTTCACCTTGAATGCTGGAATGATGATGATGATGATGATGATGATGATGATGATG 3359
Db      3121 CCACCTCTTGTCCCTGATGCGGGCGGCGGCTGTGATGATGATGATGATGATGATGATGATG 3180
Qy      3360 GGATCATTTGAAGAAACCTCTTCTGCAATGAGAAAGCAAGAGAGAGAGAGAGAGAGAGAG 3419
Db      3181 CCAATATCTCAAGAGCTCC--TGCACTGGGAGAAACAGAGAGAGAGAGAGAGAGAGAG 3237
Qy      3420 TTTGCTGGAATCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3479
Db      3238 CTTCCGAGTGAAGTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3297
Qy      3480 CTTCCAGCAGT 3491
Db      3298 GGCCCAACAAGT 3309

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RESULT 12
US-08-777-405A-1
; Sequence 1, Application us/08777405A
; Patent No. 5858753
; GENERAL INFORMATION:
; APPLICANT: Chaney, David
; APPLICANT: Hoeke, Merl F.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: No. 5858753el lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun

```

STREET: 6300 Sears Tower/233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/777,405A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 585873and, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 27866/33441
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5220 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 196..3327
 US-08-777-405A-1

Query Match 3.0%; Score 103.6; DB 2; Length 5220;
 Best Local Similarity 53.7%; Pred. No. 1.5e-21;
 Matches 264; Conservative 0; Mismatches 219; Indels 9; Gaps 2;

3000 CTCGCTGTGGATATTCAGTCCGACATTAATGGAATCAAGATCGTCACAGTGA 3059
 2826 CTCCTGTGCTGATTTGTGTGCCATATGTCTGGCGATTGGCGACAGCGCA 2885
 3060 TAATCGATGCTCAGTGAAGTGAATAATGTCACATTGATTTGGTGGG 3119
 2886 CAACATCATGATCCGAGAGAGTGGGAGCTGTTCCATTGATTTGGCCATTCTGGG 2945
 3120 ACACGGAAGACCAAACTTGGGATCCAGGAGATGCTCAACCGTTTATTCTAACCGAGACA 3179
 2946 GAATTTCAAGACCAAGTTTGAATCAACCGCGAGCTGTCCCTCATCTCATATGA 3005
 3180 CTTTATGACAGTATTCGATCGGGTAAATCTGTGATGGAATTCGATGAGCTACAAA 3239
 3006 CTTTGTCCATGTGATTCACAGGGGAA-----GACTTAATTAATGAGAAATTGAAAG 3059
 3240 ATTCAAAAGTTATGCGTGAAGCTTACGAAAGTATGTAATTCAGATTTGTTGCT 3299
 3060 GTTCCGGGGCTACTGTGAAGGCTTACACATCTCTCGCGCCAGCGGCTTCTTCT 3119
 3300 TTCTTGTTCACCTTGATGCTGGAAATGAGATTGCTGAGCTGTGACGAAAGCGGATTT 3359
 3120 CCAACCTCTTGGCCCTGATGCGGGGCGGAGCGCTGCTGAGCTGCTCCAAAGACAT 3179
 3360 GGAATCATTTGAAGAAACCTCTTTCGCAATGAGAAAGCAAGAGAGCGAGAAATT 3419
 3180 CCAATATCTCAAGACTCC--TGGCATGCGGAGAAACAGAGAGAGCGACTGAAGA 3236
 3420 TTTCGCTGAATTCAGAAAGACCTTCAATGATGATGCTTACCAAAACGATTTGGCT 3479
 3237 CTTCCGAGTGAATTTACGAAAGCCTCCGTGAGACTGGAACCAAGTGAATGCGCT 3296
 3480 CTTCAAGCAGT 3491
 3297 GGCCCAACAAGT 3308

RESULT 13
 US-08-977-871A-1
 ; Sequence 1, Application US/08977871A
 ; Patent No. 5882910
 ; GENERAL INFORMATION:
 ; APPLICANT: Chantry, David
 ; APPLICANT: Hoekstra, Merl F.
 ; APPLICANT: Holtzman, Douglas A.
 ; TITLE OF INVENTION: No. 5882910el lipid Kinase
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
 ; STREET: 6300 Sears Tower/233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/977,871A
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/777,405
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 5882910and, Greta E.
 ; REGISTRATION NUMBER: 35,302
 ; REFERENCE/DOCKET NUMBER: 27866/33441
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 474-6300
 ; TELEFAX: (312) 474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5220 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: CDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 196..3327
 ; US-08-977-871A-1

Query Match 3.0%; Score 103.6; DB 2; Length 5220;
 Best Local Similarity 53.7%; Pred. No. 1.5e-21;
 Matches 264; Conservative 0; Mismatches 219; Indels 9; Gaps 2;

3000 CTCGCTGTGGATATTCAGTCCGACATTAATGGAATCAAGATCGTCACAGTGA 3059
 2826 CTCCTGTGCTGATTTGTGTGCCATATGTCTGGCGATTGGCGACAGCGCA 2885
 3060 TAATCGATGCTCAGTGAAGTGAATAATGTCACATTGATTTGGTGGG 3119
 2886 CAACATCATGATCCGAGAGAGTGGGAGCTGTTCCATTGATTTGGCCATTCTGGG 2945
 3120 ACACGGAAGACCAAACTTGGGATCCAGGAGATGCTCAACCGTTTATTCTAACCGAGACA 3179
 2946 GAATTTCAAGACCAAGTTTGAATCAACCGCGAGCTGTCCCTCATCTCATATGA 3005
 3180 CTTTATGACAGTATTCGATCGGGTAAATCTGTGATGGAATTCGATGAGCTACAAA 3239
 3006 CTTTGTCCATGTGATTCACAGGGGAA-----GACTTAATTAATGAGAAATTGAAAG 3059
 3240 ATTCAAAAGTTATGCGTGAAGCTTACGAAAGTATGTAATTCAGATTTGTTGCT 3299

Db 3060 GTTCGGGGCTACTGTGAAGGGCCTACACCATCTCGCGCGCCACGCGCTTCTCTTCT 3119
Qy 3300 TTCTGTGTACCTTGATGCTGCGATGAGTGTGCTGAGCTGTGAGCAAGGAGATT 3359
Db 3120 CCACCTCTTTCCTGATGCTGCGCGCGCGCGCTGCTGAGCTGTGCTGCTGCTGCTGCT 3179
Qy 3360 GGATCATTTGAAGAAACCTCTTCTGCAATGAGAAAGCAAGAAAGAGAGAAAGTT 3419
Db 3180 CCAGTATCTCAAGAGCTCC--TGCACTGGGGAAGAAAGAGAGAGAGAGAGAGAGCA 3236
Qy 3420 TTTCCTGGAATCTCAAGAGAGCTTCAATGATGATGCTTACCAAAAGCAATTGGCT 3479
Db 3237 CTTCGAGTGAAGTTTAAAGAAAGCCCTCGTGAAGCTGGAAGAAACCAAGTGAAGCT 3296
Qy 3480 CTTCCAGCAGT 3491
Db 3297 GGCCCAACAGT 3308

RESULT 14

US-09-225-951-1

Sequence 1, Application US/09225951

Patent No. 5985589

GENERAL INFORMATION:

APPLICANT: Chantry, David

APPLICANT: Hoekstra, Merl F.

APPLICANT: Holzman, Douglas A

TITLE OF INVENTION: No. 5985589el Lipid Kinase

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun

STREET: 6300 Sears Tower/233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/225,951

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: No. 5985589and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27866/3441

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 5220 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 196..3327

US-09-225-951-1

Query Match 3.0%; Score 103.6; DB 2; Length 5220;

Best Local Similarity 53.7%; Pred.No. 1.5e-21;

Matches 264; Conservative 0; Mismatches 219; Indels 9; Gaps 2;

Qy 3000 CTCGCTGTGATTTTCAAGTTCACGACGACATATGGAATCAAGAGTTCACAGGCA 3059
Db 2826 CTCGCTGTGATTTTGTGCGCACATATGTCTGGGCAATTGGCGATCGCACAGGCA 2885

Qy 3060 TAATCTAGTCTCACTGAAGATGGAATAATGTCCATATTGTTTCGTACATTTTGGG 3119
Db 2886 CAACATCATGATCCGAGAGATGGGACAGCTGTTCACATTTGATTTTGGCACTTTCTGGG 2945
Qy 3120 ACACGAAAGACCAAACTTTGGATTCACAGATGATGTCACACGTTTATTTCAACGACA 3179
Db 2946 GAATTTCAAGACCAAGTTTGGATTCACACGAGCGGTGTCCATTCATTCACCTATGA 3005
Qy 3180 CTTTATGACAGTATGATGAGGTAATCTGTGATGGAATAATTCGATGAGCTACAAA 3239
Db 3006 CTTTGTTCATGATGATTCAGCAGGGGA-----GACTAATTAATGATGAATTTGAACG 3059
Qy 3240 ATTCAAAAGTATGCTGCAAGGCTTCAAGATATGATGATATTCAGATTTTTCGT 3299
Db 3060 GTTCGGGGCTACTGTGAAGGGCCTTACACCATCTGCGGCGCCACGCGCTTCTTCTCT 3119
Qy 3300 TTCTGTGTACCTTGATGCTGCGATGAGTGTGCTGAGCTGTGAGCAAGGAGATT 3359
Db 3120 CCACCTCTTTCCTGATGCTGCGCGCGCGCGCTGCTGAGCTGAGCTGCTGCTGCTGCTGCT 3179
Qy 3360 GGATCATTTGAAGAAACCTCTTCTGCAATGAGAAAGCAAGAAAGAGAGAAAGTT 3419
Db 3180 CCAGTATCTCAAGAGCTCC--TGCACTGGGGAAGAAAGAGAGAGAGAGAGAGAGCA 3236
Qy 3420 TTTCCTGGAATCTCAAGAGAGCTTCAATGATGATGCTTACCAAAAGCAATTGGCT 3479
Db 3237 CTTCGAGTGAAGTTTAAAGAAAGCCCTCGTGAAGCTGGAAGAAACCAAGTGAAGCT 3296
Qy 3480 CTTCCAGCAGT 3491
Db 3297 GGCCCAACAGT 3308

RESULT 15

US-08-916-917-3

Sequence 3, Application US/08916917

Patent No. 5856132

GENERAL INFORMATION:

APPLICANT: Stephens, Len

APPLICANT: Hawkins, Phillip Thomas

APPLICANT: Brabelmann, Sylvia

TITLE OF INVENTION: G-BETA-GAMMA REGULATED

TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds, LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/916,917

FILING DATE: 15-AUG-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/672,211

FILING DATE: 27-JUN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Abrams, Samuel B

REGISTRATION NUMBER: 30,605

REFERENCE/DOCKET NUMBER: 8549-0006-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-493-4935

TELEFAX: 650-493-5556

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 3808 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-916-917-3

Query Match 2.8%; Score 96.4; DB 2; Length 3808;

Best Local Similarity 51.9%; Pred. No. 2.1e-19; Mismatches 241; Indels 9; Gaps 2;

Matches 270; Conservative 0; Mismatches 241; Indels 9; Gaps 2;

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QY 2966 AGAAATATTTGAAAGTCGATCGATTCCTATCTCGTGTGTGGATATTCAGTTGCCA 3025
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2844 AAAAGTTTCAGGACGCTGGAGAGATTGTTATTCCTGTGCGGCTACTGTGGCAA 2903
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3026 CGTACATATGGGATCAAGATCGTCAAGATGATATCTGATGCTCACTGAAGATGGA 3085
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2904 CTTTGTTCGGAATAGGCGACAGACAAATGACAAATATTAATGATCTCAGAAACAGAA 2963
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3086 AATATGTCACATTTGATTTGGTCACTTTGGGACACGGAAGAACCAAACTTGGGATCC 3145
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2964 ATCTATTTCAATTTGATTTGGACACATTTCTGGGAATTAACAAAGTTTCTGGGCATTA 3023
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3146 AGCGAGATCGTCAACCGTTTATTTCTAACGGAACATTTATGACAGTATTCGATCGGTA 3205
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3024 ATAAAGAGAGGGTGCATTTGTGCTAACCCAGACTTCCTGTTGTGAT-----GGGGA 3077
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3206 AATCTGTGATGGAATTCGCATGAGCTACAAAATTCAAAAGTTATGCTGGAAGCCT 3265
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3078 CTTCTGGAAGAAGACAAAGTCTACACTTCAGAAATTTGAGATGTGCGTCAGGCTT 3137
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3266 AGGAAGTAAATGGAATTAATCGAGATTTGTCGTTTCTTGTTCACTTGATGCTGGAA 3325
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3138 ACTTACCCCTTGTCTATCAACAACTTACTGATCATCTCTTCTTCATGATGCTGATGA 3197
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3326 TGGAGTTGCTGAGCTGCGAGAAAGCGAATTTGATCATTTGAAGAAACCTCTTCT 3385
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3198 CAGGAATGCCCAAGTTAACGCAAGAAAGACATGATATACATTCGGATGCCCTC--A 3254
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3386 GCAATGGAAGAAAGCAAGAAAGAGCAAGAAAGTTTTCGCTGAATCTACGAAGAGCCT 3445
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3446 TCAATGATCATGCTTACCAAAACGAATTTGGCTTTCCA 3485
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3315 GAGACAAAGATGACCGTGCACTTAACTGTTCTTTACA 3354
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Search completed: June 6, 2003, 02:35:33
Job time : 256 secs

GenCore version 5.1.6
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OW nucleic - nucleic search, using sw model

Run on: June 6, 2003, 02:28:44 ; Search time 453 Seconds
(without alignments)
10825.561 Million cell updates/sec

Title: US-08-908-453-2

Perfect score: 3504
Sequence: 1 CGGAAGCCATGAGCTCGAG.....ACGAGTCACACTACTGCA 3504

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCIT_NEM_PUB.seq:*
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- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3504	100.0	3504	10	US-09-205-658-47
2	3504	100.0	3504	10	US-09-844-353A-47
3	103.6	3.0	3387	9	US-10-162-160-2
4	103.6	3.0	5220	9	US-10-027-591-1
5	77	2.2	5990	10	US-09-917-800A-477
6	68.6	2.0	5061	12	US-10-092-219-1
7	64	1.8	339	9	US-09-796-6592-7359
8	64	1.8	339	9	US-10-040-862-7359
9	59	1.7	326	9	US-09-796-692-7451
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11	46.8	1.3	3252	10	US-09-921-232-1
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14	42.8	1.2	2418	10	US-09-771-161A-10
15	42.2	1.2	5703	9	US-09-801-368-389
16	41.8	1.2	3281	9	US-10-114-170-85
17	41.2	1.2	4074	10	US-09-764-877-796
18	41	1.2	302	9	US-09-925-299-710
19	41	1.2	302	10	US-09-925-299-710

20	41	1.2	2620	10	US-09-925-302-205	Sequence 205, App
21	41	1.2	11812	9	US-10-239-676-210	Sequence 210, App
22	40	1.1	464	9	US-09-918-995-32689	Sequence 32689, A
23	39.4	1.1	466	9	US-09-918-995-35578	Sequence 35578, A
24	38.6	1.1	2000	9	US-09-938-842A-5006	Sequence 5006, App
25	38.6	1.1	2002	10	US-09-887-576-4	Sequence 4, Appl1
26	38.6	1.1	640681	10	US-09-790-988-1	Sequence 264, Appl1
27	38	1.1	532	9	US-10-184-644-264	Sequence 264, App
28	38	1.1	532	9	US-10-184-634-264	Sequence 264, App
29	37.8	1.1	436	9	US-09-918-995-857	Sequence 857, App
30	37.8	1.1	7864	10	US-09-834-575-805	Sequence 805, App
31	37	1.1	6071	9	US-10-239-676-78	Sequence 78, Appl1
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33	36.2	1.0	364	10	US-09-960-352-10067	Sequence 10067, A
34	36	1.0	2432	9	US-10-198-846-12893	Sequence 12893, A
35	36	1.0	4000	9	US-09-981-353-8	Sequence 8, Appl1
36	35.8	1.0	408	10	US-09-960-352-1221	Sequence 1221, App
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38	35.6	1.0	446	9	US-09-918-995-24787	Sequence 24787, A
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40	35.6	1.0	1955	9	US-09-984-271-98	Sequence 98, Appl1
41	35.6	1.0	1955	9	US-09-813-153-80	Sequence 80, Appl1
42	35.6	1.0	2550	9	US-09-813-153-65	Sequence 65, Appl1
43	35.6	1.0	2971	9	US-09-984-271-37	Sequence 37, Appl1
44	35.6	1.0	13606	9	US-10-239-676-165	Sequence 165, App
45	35.4	1.0	419	10	US-09-960-352-11234	Sequence 11234, A

ALIGNMENTS

RESULT 1

US-09-205-658-47
Sequence 47, Application US/09205658
Patent No. US20010029617A1
GENERAL INFORMATION:
APPLICANT: Ruvkun, Gary
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
FILE REFERENCE: 00786/351004
CURRENT FILING DATE: 1998-12-03
EARLIER FILING DATE: 1997-05-15
EARLIER FILING DATE: 1997-05-15
EARLIER APPLICATION NUMBER: 08/888,534
EARLIER FILING DATE: 1997-07-07
EARLIER APPLICATION NUMBER: US98/10080
EARLIER FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 328
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 47
LENGTH: 3504
TYPE: DNA
ORGANISM: Caenorhabditis elegans
US-09-205-658-47

Query Match 100.0%; Score 3504; DB 10; Length 3504;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 3504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	61	CAGATGATGTTAATTTTACATTCACACTGCAACGATGCTGAGACGCAATG	120
QY	121	CGAAGAGCCCATGCTGCTGAGACCGAGATGCGCAAGATGCTGCTCTGGAATGAA	180
DB	121	CGAAGAGCCCATGCTGCTGAGACCGAGATGCGCAAGATGCTGCTCTGGAATGAA	180

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Db 181 GGTGTGCGAGATATCATCTATGTGTCAATTCGAGAGATTATTAGTAGATTTCG 240
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Db 1321 TATGTGGGACACTGACGCTGCTCAATAATCTACAAAGAGATGCTCAATTTGCA 1380
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RESULT 2
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; Sequence 47, Application US/09844353A
; Patient No. US20020037585A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Kimura, Koutarou
; APPLICANT: Patterson, Garth
; APPLICANT: Ogg, Scott
; APPLICANT: Paradise, Suzanne
; APPLICANT: Tibesbaum, Heidi
; APPLICANT: Morris, Jason
; APPLICANT: Kowsek, Allison
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351005
; CURRENT APPLICATION NUMBER: US/09/844, 353A
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 08/857, 076
; PRIOR FILING DATE: 1997-05-15
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 3504
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-09-844-353A-47

Query Match 100.0%; Score 3504; DB 10; Length 3504;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 121 CGAAGCCATGAGTGTGAGATGATGATGATGATGATGATGATGATGATGATGATG 180
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Oy 181 GGTGTCGAGATTAATCATCATGATGATGATGATGATGATGATGATGATGATGATG 240
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Oy 241 TGTGTTCTTGAAGATGTCGAACATCGCTAGAAATCAAGATGATGATGATGATGATG 300
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Oy 301 CTTTTCGATTAATGATGCTCCGATGAAGTGGGAAATATTCCTGTAAGCCACAGATTA 360
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Oy 361 GTGTCAGACAGTTGAATTAATTTGCGCAATTAAGTTAATTAAGAGATCAACCC 420
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Oy 421 CTGTGAAATTAAGAGCTCCAGGACCTTCCCAATGCTTTTCTCTCAACAGATGATG 480
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841 CACACGTTTCTCTACGAAATGCGAAATGATGATGATGATGATGATGATGATGATGATGAT 900
901 GAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
901 GAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
961 CTTAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
961 CTTAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
1021 GTTCCGCGCAATCACTAGTCTCTCAAAAGCTATGTCGCCCAAAACCACTTACGAAACA 1080
1021 GTTCCGCGCAATCACTAGTCTCTCAAAAGCTATGTCGCCCAAAACCACTTACGAAACA 1080
1081 CATTTATGAGAGACACAGAGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 1140
1081 CATTTATGAGAGACACAGAGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 1140
1141 ACGACACCAAAACAGAGCAAGACAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 1200
1141 ACGACACCAAAACAGAGCAAGACAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 1200
1201 TCACTCAAAAGTTCACCTTGGGACCTTGAACGCAATCTTATGATACGCGCTGTGAAT 1260
1201 TCACTCAAAAGTTCACCTTGGGACCTTGAACGCAATCTTATGATACGCGCTGTGAAT 1260
1261 ATTTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
1261 ATTTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
1321 TATGAGGAGACAGTACGCTGGCATCAAAATCTACAAAGTGAATCTCAATTTGCA 1380
1321 TATGAGGAGACAGTACGCTGGCATCAAAATCTACAAAGTGAATCTCAATTTGCA 1380
1381 AAATGAAATAGGAAATGATCACTTTGATCTATATGATGATGATGATGATGATGATGATGAT 1440
1381 AAATGAAATAGGAAATGATCACTTTGATCTATATGATGATGATGATGATGATGATGATGAT 1440
1441 GATCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
1441 GATCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
1501 GGTGGGTAATATGTCCTTAACCGATGAGAGATGAACTACGACAGAGCAATTTTGA 1560
1501 GGTGGGTAATATGTCCTTAACCGATGAGAGATGAACTACGACAGAGCAATTTTGA 1560
1561 TTTCATCTGTGGGCTCTGAAACCGATGAGAGATGAACTACGACAGAGCAATTTTGA 1620
1561 TTTCATCTGTGGGCTCTGAAACCGATGAGAGATGAACTACGACAGAGCAATTTTGA 1620

1621 AGATAGGACCAACAGAGCGGTTACAAATTCATGATGATGATGATGATGATGATGATGATGAT 1680
1621 AGATAGGACCAACAGAGCGGTTACAAATTCATGATGATGATGATGATGATGATGATGATGAT 1680
1681 ATGCGAGTCAAGACATACATATCTGTCAGACACCGAATCTTGGACGAACT 1740
1681 ATGCGAGTCAAGACATACATATCTGTCAGACACCGAATCTTGGACGAACT 1740
1741 TTGAATATTAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
1741 TTGAATATTAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1800
1801 CAGATGCTTGTCAAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
1801 CAGATGCTTGTCAAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
1861 GTTGTGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
1861 GTTGTGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
1921 GATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
1921 GATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
1981 AAATGAAACCGCGAGTGTGAGAGCGCGCTTGAATTTGCTTGAAGAAAGTTCACGAGAT 2040
1981 AAATGAAACCGCGAGTGTGAGAGCGCGCTTGAATTTGCTTGAAGAAAGTTCACGAGAT 2040
2041 CGTGTGATGAAAGTTCAGTGAAGAGTGAATGAGACAGTGAAGCGCGCTCAATTC 2100
2041 CGTGTGATGAAAGTTCAGTGAAGAGTGAATGAGACAGTGAAGCGCGCTCAATTC 2100
2101 CATCTTTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160
2101 CATCTTTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160
2161 GTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2220
2161 GTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2220
2221 TGGCTGCTCCGTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2280
2221 TGGCTGCTCCGTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2280
2281 CGCGTATCTCACTTCTGATGAGCTTACCTCGTGAAGTGAAGACATCAAGATC 2340
2281 CGCGTATCTCACTTCTGATGAGCTTACCTCGTGAAGTGAAGACATCAAGATC 2340
2341 ATCACCCGACAAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2400
2341 ATCACCCGACAAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2400
2401 ATGCCAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460
2401 ATGCCAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460
2461 ATGCCAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520
2461 ATGCCAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520
2521 AAAGCATGCTCTAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2580
2521 AAAGCATGCTCTAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2580
2581 CCAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2640
2581 CCAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2640
2641 CGCGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2700
2641 CGCGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2700
2701 AACATTGATGCTGTTGAACCGTACGACAGTCTTCAATGAGAGAAATGATGAAAT 2760

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Db      2701 AACATTGATGCTGTTTGAACCCGTACGAGTCTTCCATGGAGAAATGATGGAAAT 2760
Qy      2761 ATTTGAAGTTGGCCTAATTTGTAACAATATCGATTTCAAGTTGGAAACAGATTTCTG 2820
Db      2761 ATTTGAAGTTGGCCTAATTTGTAACAATATCGATTTCAAGTTGGAAACAGATTTCTG 2820
Qy      2821 AATACAGAGATTCGAGAGATTTGATCTTCTGTTATGAAATAGTGGATTCGAAACATTC 2880
Db      2821 AATACAGAGATTCGAGAGATTTGATCTTCTGTTATGAAATAGTGGATTCGAAACATTC 2880
Qy      2881 GGAATTTGAAGATGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 2940
Db      2881 GGAATTTGAAGATGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 2940
Qy      2941 AAGATTGTAATTAATCAAGCCCAATGAAAGAAATTTTGAAGAGTGTGATCGATTTCTATAC 3000
Db      2941 AAGATTGTAATTAATCAAGCCCAATGAAAGAAATTTTGAAGAGTGTGATCGATTTCTATAC 3000
Qy      3001 TCGTGTGTTGATATTTCAAGTTGCCAGTACATATAGGGAATCAAGGATCGTCAAGTAT 3060
Db      3001 TCGTGTGTTGATATTTCAAGTTGCCAGTACATATAGGGAATCAAGGATCGTCAAGTAT 3060
Qy      3061 AATCTGATGCTCACTGAAAGATGAAATATATGTCACATTTGATTTGGTCAATTTTGGGA 3120
Db      3061 AATCTGATGCTCACTGAAAGATGAAATATATGTCACATTTGATTTGGTCAATTTTGGGA 3120
Qy      3121 CACGGAAGAACCAACTTGGGATCCAGGAGATTCGTCAACCGTTATTTCTAACCGAACAC 3180
Db      3121 CACGGAAGAACCAACTTGGGATCCAGGAGATTCGTCAACCGTTATTTCTAACCGAACAC 3180
Qy      3181 TTTATGACAGTATTCGATCGGGTAAATCTGTGATGGAATTTCCATGAGCTACAAAAA 3240
Db      3181 TTTATGACAGTATTCGATCGGGTAAATCTGTGATGGAATTTCCATGAGCTACAAAAA 3240
Qy      3241 TTCAAAACGTTATGCGTGCAGAGCCTTACGAAGTAATGTGGAATATCGAATTTGTCCT 3300
Db      3241 TTCAAAACGTTATGCGTGCAGAGCCTTACGAAGTAATGTGGAATATCGAATTTGTCCT 3300
Qy      3301 TCCCTGTTCACTTGTATGCTCGGAATGGAATGCTGCTGAGCTGTCCAGCAAGGAGATTTG 3360
Db      3301 TCCCTGTTCACTTGTATGCTCGGAATGGAATGCTGCTGAGCTGTCCAGCAAGGAGATTTG 3360
Qy      3361 GATCATTTGGAAGAAACCTCTTCTGCAATGAGAAAGCAAGAAAGCAAGAAAGTTT 3420
Db      3361 GATCATTTGGAAGAAACCTCTTCTGCAATGAGAAAGCAAGAAAGCAAGAAAGTTT 3420
Qy      3421 TTGCTGGAATCTCAAGAAAGCCTTCAATGATCATGCTTACCAAAACGAATTTGGCTC 3480
Db      3421 TTGCTGGAATCTCAAGAAAGCCTTCAATGATCATGCTTACCAAAACGAATTTGGCTC 3480
Qy      3481 TTCCACGAGATCAACACTACTGCA 3504
Db      3481 TTCCACGAGATCAACACTACTGCA 3504

RESULT 3
US-10-162-160-2
; Sequence 2, Application US/10162160
; Publication No. US20030099627A1
; GENERAL INFORMATION:
; APPLICANT: Van Hasebroeck, Bart
; APPLICANT: Waterfield, Michael D.
; TITLE OF INVENTION: No. US20030099627A1el Lipid Kinase
; FILE REFERENCE: 2332-1-002
; CURRENT APPLICATION NUMBER: US/10/162,160
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/194,640
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: 9611460.8
; PRIOR FILING DATE: 1996-06-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 2
; LENGTH: 3387
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-162-160-2

Query Match      3.0%; Score 103.6; DB 9; Length 3387;
Best Local Similarity 53.7%; Pred. No. 1,1e-18;
Matches 264; Conservative 0; Mismatches 219; Indels 9; Gaps 2;

Qy      3000 CTCGTGTGATGATTTCAAGTTGCCAGTACATTAATGGAATCAAGATCGTCAAGTGA 3059
Db      2631 CTCCTGTCTGCTATTTGTGTGGCCACATATGTGCTGGCATTTGGCCATCGGCA CAGCGA 2690
Qy      3060 TAATCTGATGCTCACTGAAGATGAAATATATGTCCATTTGATTTGGTCAATTTGGG 3119
Db      2631 CAACATCAATGATCCAGAGAGTGGGACAGCTGTCCACATTAATTTTGGCCATTTCTGGG 2750
Qy      3120 ACACGAAAGAACCAACTTGGGATCCAGGAGATTCGCAACCGTTATTTCTAACCGAACAC 3179
Db      2751 GAATTTCAAGCAAGTTTGAATCAACCGAGAGGTGTCCATTTCACTCACTACGA 2810
Qy      3180 CTTATGACAGTATTCGATCGGGTAAATCTGTGATGGAATTTGCAATGAGCTACAAA 3239
Db      2811 CTTTGTCCATGATGATTTCAAGAGGGGAA-----GACTAATTAATGTGAAATTTGAAAG 2864
Qy      3240 ATTCAAAACGTTATGCGTGCAGAGCCTTACGAAGTAATGTGAAATATCGAATTTGCT 3299
Db      2865 GTTCGGGGCTATGTTGTAAGAGGGCTTACCAATCTGTGGGGCCACGCGGCTTCTTCT 2924
Qy      3300 TTCTTGTTCACCTTGTATGCTCGGAATGGAATGCTGAGCTGTGACGAAAGCGGATTT 3359
Db      2925 CCACCTCTTGTGCTGATGCGGGGCGGAGGCTGTGCTGATGCTCAAGTCAAGAT 2984
Qy      3360 GGATCATTTGAAAGAAACCTCTTCTGCAATGAGAAAGCAAGAAAGCAAGAAAGTT 3419
Db      2985 CCAGATATCTCAAGAGCTCC--TGCGACTGGGGGAAACAGAGGAGAGGCACTGAACGA 3041
Qy      3420 TTGCTGGAATCTCAAGAAAGCCTTCAATGATCATGATGCTTACCAAAACGAATTTGCT 3479
Db      3042 CTTCCGAGTGAAGTTTAAAGAAAGCCTTCCGTGAGAGCTGGAAGAAACGAAGTGAAGT 3101
Qy      3480 CTTCCAGCAGCT 3491
Db      3102 GCCCCACAGCT 3113

RESULT 4
US-10-027-591-1
; Sequence 1, Application US/10027591
; Patent No. US20020161014A1
; GENERAL INFORMATION:
; APPLICANT: SADHU, Chanchal et al.
; TITLE OF INVENTION: INHIBITORS OF HUMAN PHOSPHATIDYLINOSITOL 3-KINASE DELTA
; FILE REFERENCE: 27866/36170C
; CURRENT APPLICATION NUMBER: US/10/027,591
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/841,341
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/199,655
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 60/238,057
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5220
; TYPE: DNA
; ORGANISM: Human p110delta complete cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (196)..(3327)
US-10-027-591-1

```


TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(5058)
OTHER INFORMATION:
US-10-092-219-1

Query Match 2.0% Score 68.6; DB 12; Length 5061;
Best Local Similarity 51.9%; Pred. No. 1.9e-08;
Matches 179; Conservative 0; Mismatches 164; Indels 2; Gaps 1;

QY 2865 GATTGGAACATCGGAATTTGAAGATGAAAGAAAGCAAAAGSACTACCA 2924
DB 3565 GCTTCGATACCCCTCAGGAAATCCAACTGGAATTTGGTACAGATCCTTAAAGT 3624
QY 2925 AATTCATCGAAAAGAAATGATTAATCTCAAGCCATGAAAGAAATTTGAAAGTGT 2984
DB 3625 AACCACCTTGACAGATGCTAAAGAAATACATCCCTCGAAGAAATATGAAAGGCT 3684
QY 2985 CGATCGA--TTCCATACCTCGGTGGATTAATGAGTTGCCAGTACATATGGGATC 3042
DB 3685 TCAGGAACCTTATTTATTCCTGCTGAGTGTGTAGCCACTATGTTTAAAGCATC 3744
QY 3043 AAGATCCGTCACAGTATTAATCTGATGCTCACTGAAGATGAAATATGTCACATTTAT 3102
DB 3745 TGTATGACACAAATGACATATATGCTTGAAGACAGGAGACATGTTTCACTTAC 3804
QY 3103 TTCGTCATATTTGGGACACGGAACCAAACTTGGATTCAGCGAGATGTCACCG 3162
DB 3805 TTTGGAAGTTTGGGACATGACAGATGTTTGGCAGCTTCAAAAGGAGTGGGCTCCT 3864
QY 3163 TTATTTCAACGGAACCTTATGACAGTATTCATGGGTTAA 3207
DB 3865 TTGTGCTGACCTCTGATATGGCATATGTCATTAAATGGGGTGAA 3909

RESULT 7

US-09-796-692-7359/C
Sequence 7359, Application US/09796692
Publication No. US20020198362A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: US/09/796,692
PRIOR FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 60/223,378

PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7359
LENGTH: 339
TYPE: DNA
ORGANISM: Homo sapiens
US-09-796-692-7359

Query Match 1.8% Score 64; DB 9; Length 339;
Best Local Similarity 58.3%; Pred. No. 6.6e-08;
Matches 112; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 2610 TGCATGATCTTCAAGATGAGACGATCTGCGCAGACATGCTTGTCTCAAGTCT 2669
DB 193 TGAGTGTATTTTAAATATGATGATTTACGACAGATATGTTGACATCCCAATGTT 134
QY 2670 CGAAGTTATGATTAACATCTGGAAGGCTGCAAACTGATGCTGTTGAACCCGTACGC 2729
DB 133 GCGCTGATGATTTACTCTGAAAGAGCTGTTGATCTTGGATGTTGCCCTATGG 74
QY 2730 AGTTCTTCATGAGGAGAAATGATGGAATTAATGAAATGTCCTAATGTAACAT 2789
DB 73 CTGTTAGCAACAGAGATCGCTCTGCGCTCATTTGAAGTTGAGCACCTTGAAACAT 14
QY 2790 AATGAGATTC 2801
DB 13 TGCTGACATTC 2

RESULT 8

US-10-040-862-7359/C
Sequence 7359, Application US/10040862
Publication No. US20030078396A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
FILE REFERENCE: 014058-013520US
CURRENT APPLICATION NUMBER: US/10/040,862
PRIOR FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: US 60/223,378
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: US 09/796,692
PRIOR FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 7359
LENGTH: 339
TYPE: DNA
ORGANISM: Homo sapiens
US-10-040-862-7359

Query Match 1.8%; Score 64; DB 9; Length 339;

Best Local Similarity 58.3%; Pred. No. 6,6e-08; Mismatches 80; Indels 0; Gaps 0;

Matches 112; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 2610 TGCATGATCTTCAAGATGAGAGAGATCTTCCGAGACATGCTGTTCTCAAGTTCT 2669
DB 133 TGGAGTGATTTTAAAAATGATGATATTACGACAGATATGTTGACACTCCAAATGTT 134
QY 2670 CGAAGTTATGATTAACATCTGGAGGCTGCAACATTGCTGTTTGAACCCGTACGC 2729
DB 133 GCGCTTGATGATTTACTCTGGAAGAGAGCTGTTGATCTTCGATCTTCCTTATG 74
QY 2730 AGTTCTCCATGGAGAAATGATGATTTGATTTGAGTTGCTTAATTGTAACAAT 2789
DB 73 CTGTTTACACAGAGAGATGCTCTGGCTCATTTGAGTTGAGACACTCTGAACAAT 14
QY 2790 ATTCGATGATCA 2801
DB 13 TCGTGACATTCA 2

RESULT 9

US-09-796-692-7451/c

Sequence 7451, Application US/09796692

Publication No. US20020198362A1

GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander

APPLICANT: Algate, Paul A.

APPLICANT: Mannion, Jane

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY

FILE REFERENCE: 2077.001200

CURRENT APPLICATION NUMBER: US/09/796,692

PRIOR FILING DATE: 2001-03-01

PRIOR APPLICATION NUMBER: 60/186,126

PRIOR FILING DATE: 2000-03-01

PRIOR APPLICATION NUMBER: 60/190,479

PRIOR FILING DATE: 2000-03-17

PRIOR APPLICATION NUMBER: 60/200,545

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: 60/200,303

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: 60/200,779

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: 60/200,999

PRIOR FILING DATE: 2000-05-01

PRIOR APPLICATION NUMBER: 60/202,084

PRIOR FILING DATE: 2000-05-04

PRIOR APPLICATION NUMBER: 60/206,201

PRIOR FILING DATE: 2000-05-22

PRIOR APPLICATION NUMBER: 60/218,950

PRIOR FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: 60/222,903

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: 60/223,416

PRIOR FILING DATE: 2000-08-04

PRIOR APPLICATION NUMBER: 60/223,378

PRIOR FILING DATE: 2000-08-07

NUMBER OF SEQ ID NOS: 9597

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 7451

LENGTH: 326

TYPE: DNA

ORGANISM: Homo sapiens

US-09-796-692-7451

Query Match 1.7%; Score 59; DB 9; Length 326;

Best Local Similarity 58.1%; Pred. No. 1.8e-06; Mismatches 104; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 2610 TGCATGATCTTCAAGATGAGAGATCTTCCGAGACATGCTGTTCTTCAAGTTCT 2669
DB 180 TGGAGTGATTTTAAAAATGATGATATTACGACAGATATGTTGACACTCCAAATGTT 121
QY 2670 CGAAGTTATGATTAACATCTGGAGGCTGCAACATTGCTGTTTGAACCCGTACGC 2729
DB 120 GCGCTTGATGATTTACTCTGGAAGAGAGCTGTTGATCTTCGATCTTCCTTATG 61
QY 2730 AGTTCTCCATGGAGAAATGATGATTTGATTTGAGTTGCTTAATTGTAACAAT 2789
DB 60 CTGTTTACACAGAGATGCTCTGGCTCATTTGAGTTGAGACACTCTGAACAAT 2

RESULT 10

US-10-040-862-7451/c

Sequence 7451, Application US/10040862

Publication No. US20030078396A1

GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander

APPLICANT: Algate, Paul A.

APPLICANT: Mannion, Jane

APPLICANT: Retter, Marc

APPLICANT: Corixa Corporation

TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy

FILE REFERENCE: 014058-013520US

CURRENT APPLICATION NUMBER: US/10/040,862

PRIOR FILING DATE: 2001-11-06

PRIOR APPLICATION NUMBER: 60/186,126

PRIOR FILING DATE: 2000-03-01

PRIOR APPLICATION NUMBER: 60/190,479

PRIOR FILING DATE: 2000-03-17

PRIOR APPLICATION NUMBER: 60/200,545

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: 60/200,303

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: 60/200,779

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: 60/200,999

PRIOR FILING DATE: 2000-05-01

PRIOR APPLICATION NUMBER: 60/202,084

PRIOR FILING DATE: 2000-05-04

PRIOR APPLICATION NUMBER: 60/206,201

PRIOR FILING DATE: 2000-05-22

PRIOR APPLICATION NUMBER: 60/218,950

PRIOR FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: 60/222,903

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: 60/223,416

PRIOR FILING DATE: 2000-08-04

PRIOR APPLICATION NUMBER: 60/223,378

PRIOR FILING DATE: 2000-08-07

PRIOR APPLICATION NUMBER: 60/223,378

PRIOR FILING DATE: 2001-03-01

NUMBER OF SEQ ID NOS: 10467

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 7451

LENGTH: 326

TYPE: DNA

ORGANISM: Homo sapiens

US-10-040-862-7451

Query Match 1.7%; Score 59; DB 9; Length 326;
Best Local Similarity 58.1%; Pred. No. 1.8e-06;
Matches 104; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 2610 TGCATGATCTTCAAGATGAGAGATCTTCCGAGACATGCTGTTCTTCAAGTTCT 2669
DB 180 TGGAGTGATTTTAAAAATGATGATATTACGACAGATATGTTGACACTCCAAATGTT 121

Qy 2670 GCAAGTATGATACATCTGGAGAGCTGCMAAATGATTCGTGTGGAACCGGTACGC 2729
 Db 120 GCGCTTGATGATTTACTGTGAAGAAGCTGGTTTGATCTTCGGATCTTCCTTATG 61
 Qy 2730 ACTTTTTCATGGAGAAATGATTTGGAATTTTGAAGTTGGCTTAATTTGAAACAA 2788
 Db 60 CTGTTTACCAACAGAGATCGCTCTGGCTTCAATGAAGTTGTGAGACACTCTGAACA 2

RESULT 11

US-09-921-232-1
 ; Sequence 1, Application US/09921232
 ; Patent No. US20020102681A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Martino-Catt, Susan J.
 ; APPLICANT: Wang, Hongyu R.
 ; TITLE OF INVENTION: Polypeptides Controlling Phytate
 ; FILE REFERENCE: 0706D4
 ; CURRENT APPLICATION NUMBER: US/09/921,232
 ; PRIOR FILING DATE: 2001-08-02
 ; PRIOR APPLICATION NUMBER: 60/055,446
 ; PRIOR FILING DATE: 1997-08-11
 ; PRIOR APPLICATION NUMBER: 60/055,526
 ; PRIOR FILING DATE: 1997-08-08
 ; PRIOR APPLICATION NUMBER: 60/053,944
 ; PRIOR FILING DATE: 1997-07-28
 ; PRIOR APPLICATION NUMBER: 09/118,442
 ; PRIOR FILING DATE: 1998-07-17
 ; PRIOR APPLICATION NUMBER: 09/677,064
 ; PRIOR FILING DATE: 2000-09-29
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 3252
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (258)...(2666)
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(3252)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-921-232-1

Query Match 1.3%; Score 46.8; DB 10; Length 3252;
 Best Local Similarity 57.5%; Pred. No. 0.027;
 Matches 84; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 2976 TGAAGTGTGATGATTCCTTACTCGTGTGATGATTTGATTCGACGTACATAT 3035
 Db 2168 TCAATGTTGGAGACATTCATTAAGCTGCGCGTTACTGTTCATTACATATAT 2227
 Qy 3036 GGGATCAAGATCTCAAGATATATCTGATGCTCACTGAAGATGAAATATATGCA 3095
 Db 2228 GGGGGTGGAGACAGCATCTGATATATCTTCTTAAGTATGATGACGCGCTTTTCA 2287
 Qy 3096 CATGATTTGGTCAATTTTGGGAC 3121
 Db 2288 TGTGACTTTGCTTTATCTCTTGGG 2313

RESULT 12

US-09-921-330-1
 ; Sequence 1, Application US/09921330
 ; Patent No. US20020102682A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Martino-Catt, Susan J.
 ; APPLICANT: Wang, Hongyu R.
 ; APPLICANT: Beach, Larry R.
 ; TITLE OF INVENTION: Polypeptides Controlling Phytate
 ; TITLE OF INVENTION: Metabolism in Plants

FILE REFERENCE: 0706D3
 ; CURRENT APPLICATION NUMBER: US/09/921,330
 ; CURRENT FILING DATE: 2001-08-02
 ; PRIOR APPLICATION NUMBER: 60/055,446
 ; PRIOR FILING DATE: 1997-08-11
 ; PRIOR APPLICATION NUMBER: 60/055,526
 ; PRIOR FILING DATE: 1997-08-08
 ; PRIOR APPLICATION NUMBER: 60/053,944
 ; PRIOR FILING DATE: 1997-07-28
 ; PRIOR APPLICATION NUMBER: 09/118,442
 ; PRIOR FILING DATE: 1998-07-17
 ; PRIOR APPLICATION NUMBER: 09/677,064
 ; PRIOR FILING DATE: 2000-09-29
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 3252
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (258)...(2666)
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(3252)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-921-330-1

Query Match 1.3%; Score 46.8; DB 10; Length 3252;
 Best Local Similarity 57.5%; Pred. No. 0.027;
 Matches 84; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 2976 TGAAGTGTGATGATTCCTTACTCGTGTGATGATTTGATTCGACGTACATAT 3035
 Db 2168 TCAATGTTGGAGACATTCATTAAGCTGCGCGTTACTGTTCATTACATATAT 2227
 Qy 3036 GGGATCAAGATCTCAAGATATATCTGATGCTCACTGAAGATGAAATATATGCA 3095
 Db 2228 GGGGGTGGAGACAGCATCTGATATATCTTCTTAAGTATGATGACGCGCTTTTCA 2287
 Qy 3096 CATGATTTGGTCAATTTTGGGAC 3121
 Db 2288 TGTGACTTTGCTTTATCTCTTGGG 2313

RESULT 13

US-09-921-329-1
 ; Sequence 1, Application US/09921329
 ; Patent No. US20020110884A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Martino-Catt, Susan J.
 ; APPLICANT: Wang, Hongyu R.
 ; TITLE OF INVENTION: Polypeptides Controlling Phytate
 ; TITLE OF INVENTION: Metabolism in Plants
 ; FILE REFERENCE: 0706D2
 ; CURRENT APPLICATION NUMBER: US/09/921,329
 ; PRIOR FILING DATE: 2001-08-02
 ; PRIOR APPLICATION NUMBER: 60/055,446
 ; PRIOR FILING DATE: 1997-08-11
 ; PRIOR APPLICATION NUMBER: 60/055,526
 ; PRIOR FILING DATE: 1997-08-08
 ; PRIOR APPLICATION NUMBER: 60/053,944
 ; PRIOR FILING DATE: 1997-07-28
 ; PRIOR APPLICATION NUMBER: 09/118,442
 ; PRIOR FILING DATE: 1998-07-17
 ; PRIOR APPLICATION NUMBER: 09/677,064
 ; PRIOR FILING DATE: 2000-09-29
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 3252
 ; TYPE: DNA
 ; ORGANISM: Zea mays

FEATURE:
 NAME/KEY: CDS
 LOCATION: (258)...(2666)
 NAME/KEY: misc_feature
 LOCATION: (1)...(3252)
 OTHER INFORMATION: n = A,T,C or G
 US-09-921-329-1

Query Match 1.3%; Score 46.8; DB 10; Length 3252;
 Best Local Similarity 57.5%; Pred. No. 0.027;
 Matches 84; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 2976 TGAAGTGCATGCTGCTTACCGGTGGATGATTCAGTTGCCACGACATAT 3035
 DB 2168 TCATGTTTGAGACATTTATAAAGCTGCCCGGTACTCTGTCATTACATCAAT 2227
 QY 3036 GGAATCAAGATCGTCACAGTATATCTGCTACTGAAGTGAATAATGTCCA 3095
 DB 2228 GGGGGTTGAGACAGGCACTGATATCTTCTTCACTGATGAGCGCTTTTCA 2287
 QY 3096 CATGATTTGGTCACTTTGGGAC 3121
 DB 2288 TGTGACTTTCCTTATCTCTGGGC 2313

RESULT 14

US-09-771-161A-10
 Sequence 10, Application US/09771161A
 Patent No. US2002011081A1
 GENERAL INFORMATION:

APPLICANT: LEVINE, et al.
 TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
 FILE REFERENCE: 802620-2005.1
 CURRENT APPLICATION NUMBER: US/09/771,161A
 CURRENT FILING DATE: 2001-01-26
 PRIOR APPLICATION NUMBER: 09/724,676
 PRIOR FILING DATE: 2000-11-28
 PRIOR APPLICATION NUMBER: 136776
 PRIOR FILING DATE: 2000-06-15
 PRIOR APPLICATION NUMBER: 135619
 PRIOR FILING DATE: 2000-04-12
 NUMBER OF SEQ ID NOS: 273
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 10
 LENGTH: 2418
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-771-161A-10

Query Match 1.2%; Score 42.8; DB 10; Length 2418;
 Best Local Similarity 53.6%; Pred. No. 0.32; 77; Indels 0; Gaps 0;
 Matches 89; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 2608 TGTGCAATGATCTTCAAGATGAGACATCTTCCAGACATGCTGTTCTTCAAGTT 2667
 DB 1938 TATCCAGTATATTTAAGATGAGATGATTTAAGTCAAGATCACTTATCTTCAATC 1997
 QY 2668 CTCGAAGTATGATTAACATCTGGAAGCTGCAACATGATGCTGTTGAACCGTAC 2727
 DB 1998 ATTTCACATGACACAGCTGTTACGGAAGAAATCTGACTTGAATTTGACACCTTAT 2057
 QY 2728 GCAGTCTTCCAAATGGGAAATGATTTGAATTTATGAACTGTGC 2773
 DB 2058 AAGGTGTAGCCACAGTACAAAACATGCTTCATGACGTTATTC 2103

RESULT 15

US-09-801-368-389
 Sequence 389, Application US/09801368
 Patent No. US20020128250A1
 GENERAL INFORMATION:
 APPLICANT: Busby, Robert
 APPLICANT: Cali, Brian

APPLICANT: Hecht, Peter
 APPLICANT: Holtzman, Doug
 APPLICANT: Madden, Kevin
 APPLICANT: Maxon, Mary
 APPLICANT: Milne, Todd
 APPLICANT: No. US20020128250A1man, Thea
 APPLICANT: Royer, John
 APPLICANT: Salama, Sofie
 APPLICANT: Sherman, Amir
 APPLICANT: Silva, Jeff
 APPLICANT: Summers, Eric
 TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
 FILE REFERENCE: 109272.147
 CURRENT APPLICATION NUMBER: US/09/801,368
 PRIOR APPLICATION NUMBER: US 09/487,558
 PRIOR FILING DATE: 2000-01-19
 PRIOR APPLICATION NUMBER: US 60/160,587
 PRIOR FILING DATE: 1999-10-20
 NUMBER OF SEQ ID NOS: 440
 SOFTWARE: Patentin version 3.0
 SEQ ID NO 389
 LENGTH: 5703
 TYPE: DNA
 ORGANISM: Saccharomyces cerevisiae
 US-09-801-368-389

Query Match 1.2%; Score 42.2; DB 10; Length 5703;
 Best Local Similarity 58.3%; Pred. No. 0.84;
 Matches 74; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 2992 TTCCTATCTGCTGTTGATATTCAGTTGCCAGTCAATPAATGGAAATCAAGATGCT 3051
 DB 5206 TTGTTAATCTTATGCGGATATAGCGTAATTTGTAATTTGTTGCAATTCAGGATAGA 5265
 QY 3052 CACAGTGAATATCTGATCTGCTGACAGATGGAATAATGTCCACATTTGATTTCCGTAC 3111
 DB 5266 CATATGTAATATTTATGATGATGATCAAGACATTTCTACATATGATTTTGGGTTT 5325
 QY 3112 ATTTTGG 3118
 DB 5326 ATTTTGG 5332

Search completed: June 6, 2003, 05:11:19
 Job time: 503 secs